

**SEARCH REQUEST FORM**

Scientific and Technical Information Center

Requester's Full Name: \_\_\_\_\_ Examiner #: \_\_\_\_\_ Date: \_\_\_\_\_  
 Art Unit: \_\_\_\_\_ Phone Number 30 \_\_\_\_\_ Serial Number: \_\_\_\_\_  
 Mail Box and Bldg/Room Location: \_\_\_\_\_ Results Format Preferred (circle): PAPER DISK E-MAIL

If more than one search is submitted, please prioritize searches in order of need.

\*\*\*\*\*

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc. if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: \_\_\_\_\_

Inventors (please provide full names): \_\_\_\_\_

Earliest Priority Filing Date: \_\_\_\_\_

*\*For Sequence Searches Only\* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.*

\*\*\*\*\*  
**STAFF USE ONLY****Type of Search****Vendors and cost where applicable**

Searcher: <u>P. Schreiber</u>	NA Sequence (#) <u>4</u>	STN _____
Searcher Phone #: <u>272-2526</u>	AA Sequence (#) <u>1</u>	Dialog _____
Searcher Location: <u>Rensselaer 61A61</u>	Structure (#) _____	Questel/Orbit _____
Date Searcher Picked Up: <u>5/4</u>	Bibliographic _____	Dr.Link _____
Date Completed: _____	Litigation _____	Lexis/Nexis _____
Searcher Prep & Review Time: <u>14</u>	Fulltext _____	Sequence Systems <u>CompuLink</u>
Clerical Prep Time: _____	Patent Family _____	WWW/Internet _____
Online Time: <u>23</u>	Other _____	Other (specify) _____

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 1, 2004, 21:45:56 ; Search time 45 Seconds

(without alignments)  
495.609 Million cell updates/sec

Title: US-09-866-379D-10

Perfect score: 2258  
Sequence: 1 MKAILPLSLILPLTPQSA.....CSLAGFTQIVNEARIPACSL 432

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database: Issued Patents AA:\*

1: /cgm2\_6/prodata/2/1aa/5A\_COMB.pep:\*  
2: /cgm2\_6/prodata/2/1aa/5B\_COMB.pep:\*  
3: /cgm2\_6/prodata/2/1aa/5C\_COMB.pep:\*  
4: /cgm2\_6/prodata/2/1aa/5D\_COMB.pep:\*  
5: /cgm2\_6/prodata/2/1aa/5E\_COMB.pep:\*  
6: /cgm2\_6/prodata/2/1aa/5F\_COMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2171	96.1	440	3	US-09-259-214-2
2	2171	96.1	440	3	US-09-318-528-2
3	2171	96.1	440	3	US-09-291-931-2
4	2147	95.1	423	4	US-09-540-149A-1
5	2063.5	91.4	423	2	US-08-910-798-2
6	343	24.0	421	4	US-09-489-039A-7512
7	381	16.9	522	4	US-09-489-039A-13501
8	126	5.6	439	4	US-09-044-718-3
9	126	5.6	440	4	US-09-684-855-106
10	126	5.6	440	4	US-09-684-855-108
11	126	5.6	440	4	US-09-684-855-109
12	126	5.6	449	4	US-09-044-718-12
13	126	5.6	449	4	US-08-868-435-33
14	126	5.6	449	4	US-08-868-435-33
15	126	5.6	449	4	US-09-044-718-78
16	126	5.6	449	4	US-09-044-718-78
17	126	5.6	449	4	US-09-636-499-6
18	125	5.5	440	4	US-09-273-871A-8
19	125	5.5	440	4	US-09-684-855-107
20	125	5.5	440	4	US-09-684-855-109
21	124	5.5	440	4	US-09-684-855-107
22	118	5.2	440	4	US-09-684-855-108
23	118	5.2	440	4	US-09-684-855-108
24	118	5.2	440	4	US-09-684-855-108
25	118	5.2	440	4	US-09-684-855-108
26	117	5.2	440	4	US-09-044-718-79
27	116	5.1	440	4	US-09-684-855-109

28	116	5.1	440	4	US-09-684-855-131	Sequence 131, App
29	116	5.1	440	4	US-09-684-855-134	Sequence 154, App
30	116	5.1	440	4	US-09-044-718-81	Sequence 81, App
31	109.5	4.8	465	4	US-09-636-499-13	Sequence 13, App
32	109.5	4.8	479	1	US-07-923-724-2	Sequence 2, App
33	109.5	4.8	479	2	US-08-609-426A-2	Sequence 4, App
34	109.5	4.8	479	2	US-08-374-652C-4	Sequence 142, App
35	109	4.8	413	4	US-09-684-855-142	Sequence 119, App
36	109	4.8	422	4	US-09-684-855-119	Sequence 28, App
37	109	4.8	422	3	US-08-993-352-28	Sequence 28, App
38	109	4.8	442	4	US-09-273-871A-4	Sequence 28, App
39	109	4.8	442	4	US-09-482-558A-28	Sequence 14, App
40	108.5	4.8	455	4	US-09-636-499-14	Sequence 14, App
41	108	4.8	386	1	US-08-758-213-1	Sequence 1, App
42	108	4.8	386	2	US-08-692-787-48	Sequence 48, App
43	108	4.8	386	3	US-09-097-199-48	Sequence 48, App
44	108	4.8	515	2	US-09-146-283-2	Sequence 2, App
45	108	4.8	515	3	US-08-579-823A-2	Sequence 2, App

#### ALIGNMENTS

RESULT 1  
US-09-259-214-2  
Sequence 2, Application US/09259214A  
Patent No. 6110719  
GENERAL INFORMATION:  
APPLICANT: Kretz, Keith  
TITLE OF INVENTION: NOVEL PHYLASE  
FILE REFERENCE: DIVER1370-1  
CURRENT APPLICATION NUMBER: US/09/259,214A  
EARLIER FILING DATE: 1999-03-01  
EARLIER APPLICATION NUMBER: 08/910,798  
NUMBER OF SEQ ID NOS: 4  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 2  
LENGTH: 440  
TYPE: PRT  
ORGANISM: Escherichia coli  
US-09-259-214-2

Query Match 96.1%; Score 2171; DB 3; Length 440;  
Best Local Similarity 97.7%; Pred. No. 4.4e-22;  
Matches 422; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY	1	MKAILPLSLILPLTPQSAFQSEPELKSIVYVSHGVRAPKATQQLMDVTPDAMP	60
DB	1	MKAILPLSLILPLTPQSAFQSEPELKSIVYVSHGVRAPKATQQLMDVTPDAMP	60
QY	61	TPVFKLGEPLTPGSELIAVGHYMRQRLVADGLAFKCCGPOSGOVAIADVDERTKTGE	120
DB	61	TPVFKLGEPLTPGSELIAVGHYMRQRLVADGLAFKCCGPOSGOVAIADVDERTKTGE	120
QY	121	APFAGIAPCAITVTHQADTSSPDLPFPLKTVGQQLDNNAVTTALIERAGSIADEFTGH	180
DB	121	APFAGIAPCAITVTHQADTSSPDLPFPLKTVGQQLDNNAVTTALIERAGSIADEFTGH	180
QY	181	YQTAPELRLVNFPOSNLCKREKODSCSLTQALPELKVSAADVSLTGAVALASLT	240
DB	181	YQTAPELRLVNFPOSNLCKREKODSCSLTQALPELKVSAADVSLTGAVALASLT	240
QY	241	ETFLQQAQMPBPQGRITDSHQNNTLSLHNAQFDLLQTPVARSRAPELIDLIXTA	300
DB	241	ETFLQQAQMPBPQGRITDSHQNNTLSLHNAQFDLLQTPVARSRAPELIDLIXTA	300
QY	301	LTPHPQKQAYGVTLPTSVLFIAGHDITNLANGLALHNTWLLPQGPDPNTPPGSELVFERW	360
DB	301	LTPHPQKQAYGVTLPTSVLFIAGHDITNLANGLALHNTWLLPQGPDPNTPPGSELVFERW	360
QY	361	RRSDNSQWIOVSLPQTLQCMRDCTPLSINTPPEVLTLAGGEERAAQMGSLAGFTQ	420
DB	361	RRSDNSQWIOVSLPQTLQCMRDCTPLSINTPPEVLTLAGGEERAAQMGSLAGFTQ	420

Db 361 RLSDNSQWQVSLVPTLQOMRDKTPLSLNTPPGEVKLTLAGCEBNAQMGCSLAGFTQ 420  
QY 421 IYNEARIPACSL 432  
Db 421 IYNEARIPACSL 432

RESULT 2  
US-09-318-528-2  
Sequence 2, Application US/09318528  
Patent No. 6183740  
GENERAL INFORMATION:  
APPLICANT: Kretz, Keith  
TITLE OF INVENTION: NOVEL PHYTASE  
FILE REFERENCE: 09010/029003  
CURRENT APPLICATION NUMBER: US/09/318,528  
CURRENT FILING DATE: 1999-05-25  
EARLIER APPLICATION NUMBER: 09/291,931  
EARLIER FILING DATE: 1999-04-13  
EARLIER APPLICATION NUMBER: 08/910,798  
EARLIER FILING DATE: 1997-08-13  
EARLIER APPLICATION NUMBER: 09/259,214  
EARLIER FILING DATE: 1999-03-01  
NUMBER OF SEQ ID NOS: 4  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 2  
LENGTH: 440  
TYPE: PRT  
ORGANISM: Escherichia coli  
US-09-318-528-2

Query Match 96.1%; Score 2171; DB 3; Length 440;  
Best Local Similarity 97.7%; Pred. No. 4,4e-221;  
Matches 422; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 1 MKAIIIPFSLIPLTPGSAFAQSEBELKESVIVSRHGVAPTRKATQLMQDVTDPDAMP 60  
Db 1 MKAIIIPFSLIPLTPGSAFAQSEBELKESVIVSRHGVAPTRKATQLMQDVTDPDAMP 60  
QY 61 TWPVKLGELTPRGELIAYIGHYWRQRLVADGLPKGCGPQSGQVAIADVDETRKTGE 120  
Db 61 TWPVKLGELTPRGELIAYIGHYWRQRLVADGLPKGCGPQSGQVAIADVDETRKTGE 120  
QY 121 APAAGLAPDCATVHTQADTSSPDPLFNPDKTGVQCLDANANTDAILERAGGSINDFTGH 180  
Db 121 APAAGLAPDCATVHTQADTSSPDPLFNPDKTGVQCLDANANTDAILERAGGSINDFTGH 180  
QY 181 YQTAPELERVINFPOSNCLKREKODESCSLTQALPSELKVSADCVSLTGAVSLSMLT 240  
Db 181 YQTAPELERVINFPOSNCLKREKODESCSLTQALPSELKVSADCVSLTGAVSLSMLT 240  
QY 241 EIFLQQAQMPGPGGRITDSHQWNTLLSLHNAQFLLQRTPEVARSRATPLDLIKTA 300  
Db 241 EIFLQQAQMPGPGGRITDSHQWNTLLSLHNAQFLLQRTPEVARSRATPLDLIKTA 300  
QY 301 LTFHPPOKQAYGTLTFTSVLFIAGHDTNLANTGALIELNWTLPQCPDNTPPGGEIVFERW 360  
Db 301 LTFHPPOKQAYGTLTFTSVLFIAGHDTNLANTGALIELNWTLPQCPDNTPPGGEIVFERW 360  
QY 361 RLSDNSQWQVSLVPTLQOMRDKTPLSLNTPPGEVKLTLAGCEBNAQMGCSLAGFTQ 420  
Db 361 RLSDNSQWQVSLVPTLQOMRDKTPLSLNTPPGEVKLTLAGCEBNAQMGCSLAGFTQ 420  
QY 421 IYNEARIPACSL 432  
Db 421 IYNEARIPACSL 432

RESULT 3  
US-09-291-931-2  
Sequence 2, Application US/09291931A  
Patent No. 6190897  
GENERAL INFORMATION:

APPLICANT: Kretz, Keith  
TITLE OF INVENTION: NOVEL PHYTASE  
FILE REFERENCE: 09010/029003  
CURRENT APPLICATION NUMBER: US/09/291,931A  
CURRENT FILING DATE: 1999-04-13  
EARLIER APPLICATION NUMBER: 08/910,798  
EARLIER FILING DATE: 1997-08-13  
EARLIER APPLICATION NUMBER: 09/259,214  
EARLIER FILING DATE: 1999-03-01  
NUMBER OF SEQ ID NOS: 4  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 2  
LENGTH: 440  
TYPE: PRT  
ORGANISM: Escherichia coli  
US-09-291-931-2

Query Match 96.1%; Score 2171; DB 3; Length 440;  
Best Local Similarity 97.7%; Pred. No. 4,4e-221;  
Matches 422; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 1 MKAIIIPFSLIPLTPGSAFAQSEBELKESVIVSRHGVAPTRKATQLMQDVTDPDAMP 60  
Db 1 MKAIIIPFSLIPLTPGSAFAQSEBELKESVIVSRHGVAPTRKATQLMQDVTDPDAMP 60  
QY 61 TWPVKLGELTPRGELIAYIGHYWRQRLVADGLPKGCGPQSGQVAIADVDETRKTGE 120  
Db 61 TWPVKLGELTPRGELIAYIGHYWRQRLVADGLPKGCGPQSGQVAIADVDETRKTGE 120  
QY 121 APAAGLAPDCATVHTQADTSSPDPLFNPDKTGVQCLDANANTDAILERAGGSINDFTGH 180  
Db 121 APAAGLAPDCATVHTQADTSSPDPLFNPDKTGVQCLDANANTDAILERAGGSINDFTGH 180  
QY 181 YQTAPELERVINFPOSNCLKREKODESCSLTQALPSELKVSADCVSLTGAVSLSMLT 240  
Db 181 YQTAPELERVINFPOSNCLKREKODESCSLTQALPSELKVSADCVSLTGAVSLSMLT 240  
QY 241 EIFLQQAQMPGPGGRITDSHQWNTLLSLHNAQFLLQRTPEVARSRATPLDLIKTA 300  
Db 241 EIFLQQAQMPGPGGRITDSHQWNTLLSLHNAQFLLQRTPEVARSRATPLDLIKTA 300  
QY 301 LTFHPPOKQAYGTLTFTSVLFIAGHDTNLANTGALIELNWTLPQCPDNTPPGGEIVFERW 360  
Db 301 LTFHPPOKQAYGTLTFTSVLFIAGHDTNLANTGALIELNWTLPQCPDNTPPGGEIVFERW 360  
QY 361 RLSDNSQWQVSLVPTLQOMRDKTPLSLNTPPGEVKLTLAGCEBNAQMGCSLAGFTQ 420  
Db 361 RLSDNSQWQVSLVPTLQOMRDKTPLSLNTPPGEVKLTLAGCEBNAQMGCSLAGFTQ 420  
QY 421 IYNEARIPACSL 432  
Db 421 IYNEARIPACSL 432

RESULT 4  
US-09-540-149A-1  
Sequence 1, Application US/09540149A  
Patent No. 651699  
GENERAL INFORMATION:  
APPLICANT: Lei, Xingren  
TITLE OF INVENTION: ENZYMES WITH IMPROVED PHYTASE ACTIVITY  
FILE REFERENCE: 19603/2791  
CURRENT APPLICATION NUMBER: US/09/540,149A  
CURRENT FILING DATE: 2000-03-31  
PRIOR APPLICATION NUMBER: 60/127,032  
PRIOR FILING DATE: 1998-03-31  
NUMBER OF SEQ ID NOS: 9  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 1  
LENGTH: 433  
TYPE: PRT  
ORGANISM: Escherichia coli  
FEATURE:

Tue May 4 07:05:29 2004

us-09-866-379d-10.ra1

Page 3

NAME/KEY: UNSURE  
LOCATION: (433)  
OTHER INFORMATION: Xaa at position 433 in this sequence is unknown  
US-09-540-149A-1

Query Match 95.1%; Score 2147; DB 4; Length 433;  
Best Local Similarity 96.8%; Pred. No. 1.5e-218;  
Matches 418; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 1 MKALIPPLSLIPLTPQSAFAPQSEPELKESVIVSRHGVRAPTKATQMODVTPDAMP 60  
DB 1 MKALIPPLSLIPLTPQSAFAPQSEPELKESVIVSRHGVRAPTKATQMODVTPDAMP 60  
QY 61 TWPVKGLTPRGELIAYLGHYRQRLVADGLPKCGCPQSGQVAILADVDETRKTGE 120  
DB 61 TWPVKGLTPRGELIAYLGHYRQRLVADGLPKCGCPQSGQVAILADVDETRKTGE 120  
QY 121 APAAGLAPDCAITVHTQADTSSPDLFNPPLKTVGCQLDANAVTDAILSRAGSIADEFTH 180  
DB 121 APAAGLAPDCAITVHTQADTSSPDLFNPPLKTVGCQLDANAVTDAILSRAGSIADEFTH 180  
QY 181 YOTAFRELERVINFPSNCLKREKODESCSLTQALPSELKVSADCVSLTGAVSLASMLT 240  
DB 181 ROTAFRELERVINFPSNCLKREKODESCSLTQALPSELKVSADCVSLTGAVSLASMLT 240  
QY 241 EIFLLQQAQMPGPGWGRITDSHQWNTLLSLHNAQFDLLQRTPEVARSRATPLDLIMAA 300  
DB 241 EIFLLQQAQMPGPGWGRITDSHQWNTLLSLHNAQFDLLQRTPEVARSRATPLDLIMAA 300  
QY 301 LTPHPKQKAYGVTLPTSVLFIAGHDTNLANLGALELNTLPGQPDNTPPGSELVFERW 360  
DB 301 LTPHPKQKAYGVTLPTSVLFIAGHDTNLANLGALELNTLPGQPDNTPPGSELVFERW 360  
QY 361 RLSDNSQMIQVSLVPTQLQWEDKTPLSLNTPPGEVKTLTLAGCEERNAQMGSLAGFTQ 420  
DB 361 RLSDNSQMIQVSLVPTQLQWEDKTPLSLNTPPGEVKTLTLAGCEERNAQMGSLAGFTQ 420  
QY 421 IYNEARIPACSL 432  
DB 421 IYNEARIPACSL 432

RESULT 5  
US-08-910-798-2

Sequence 2, Application US/08910798  
Patent No. 5876997  
GENERAL INFORMATION:  
APPLICANT: KRETZ  
TITLE OF INVENTION: NOVEL PHYTASE  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson P.C.  
CITY: La Jolla  
STATE: California  
COUNTRY: US  
ZIP: 92037  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/910,798  
FILING DATE: August 13, 1997  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: HAILE, PH.D., LISA A.  
REGISTRATION NUMBER: 38,347  
REFERENCE/DOCKET NUMBER: 09010/029001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 619/678-5070  
TELEFAX: 619/678-5099

INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 423 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-910-798-2

Query Match 91.4%; Score 2063.5; DB 2; Length 423;  
Best Local Similarity 93.8%; Pred. No. 1e-209;  
Matches 405; Conservative 0; Mismatches 10; Indels 17; Gaps 1;

QY 1 MKALIPPLSLIPLTPQSAFAPQSEPELKESVIVSRHGVRAPTKATQMODVTPDAMP 60  
DB 1 MKALIPPLSLIPLTPQSAFAPQSEPELKESVIVSRHGVRAPTKATQMODVTPDAMP 60  
QY 61 TWPVKGLTPRGELIAYLGHYRQRLVADGLPKCGCPQSGQVAILADVDETRKTGE 120  
DB 61 TWPVKGLTPRGELIAYLGHYRQRLVADGLPKCGCPQSGQVAILADVDETRKTGE 119  
QY 121 APAAGLAPDCAITVHTQADTSSPDLFNPPLKTVGCQLDANAVTDAILSRAGSIADEFTH 180  
DB 120 -----CAUTSSPDLFNPPLKTVGCQLDANAVTDAILSRAGSIADEFTH 163  
QY 181 YOTAFRELERVINFPSNCLKREKODESCSLTQALPSELKVSADCVSLTGAVSLASMLT 240  
DB 164 ROTAFRELERVINFPSNCLKREKODESCSLTQALPSELKVSADCVSLTGAVSLASMLT 223  
QY 241 EIFLLQQAQMPGPGWGRITDSHQWNTLLSLHNAQFDLLQRTPEVARSRATPLDLIMAA 300  
DB 224 EIFLLQQAQMPGPGWGRITDSHQWNTLLSLHNAQFDLLQRTPEVARSRATPLDLIMAA 283  
QY 301 LTPHPKQKAYGVTLPTSVLFIAGHDTNLANLGALELNTLPGQPDNTPPGSELVFERW 360  
DB 284 LTPHPKQKAYGVTLPTSVLFIAGHDTNLANLGALELNTLPGQPDNTPPGSELVFERW 343  
QY 361 RLSDNSQMIQVSLVPTQLQWEDKTPLSLNTPPGEVKTLTLAGCEERNAQMGSLAGFTQ 420  
DB 344 RLSDNSQMIQVSLVPTQLQWEDKTPLSLNTPPGEVKTLTLAGCEERNAQMGSLAGFTQ 403  
QY 421 IYNEARIPACSL 432  
DB 404 IYNEARIPACSL 415

RESULT 6

US-09-489-039A-7512  
Sequence 7512, Application US/09489039A  
Patent No. 6610836  
GENERAL INFORMATION:  
APPLICANT: Gary Breton et. al  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA  
PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS  
FILE REFERENCE: 2709.2004001  
CURRENT APPLICATION NUMBER: US/09/489,039A  
CURRENT FILING DATE: 2000-01-27  
PRIOR APPLICATION NUMBER: US 60/117,747  
PRIOR FILING DATE: 1999-01-29  
NUMBER OF SEQ ID NOS: 14342  
SEQ ID NO 7512  
LENGTH: 421  
TYPE: PRT  
ORGANISM: Klebsiella pneumoniae  
US-09-489-039A-7512

Query Match 24.0%; Score 543; DB 4; Length 421;  
Best Local Similarity 32.6%; Pred. No. 1.1e-48;  
Matches 136; Conservative 70; Mismatches 181; Indels 30; Gaps 10;

QY 19 SAGPQSE---PE-LKESVIVSRHGVRAP-TKATQMODVTPDAMPPTVPVLTGELTPR 72  
DB 23 SAGPQADPKAPEGVQLQVLTIMSRHRLAPLANNGSVLEOSTAKAWPQMDVPGGLTTK 82



QY 73 GGEIAYIGHYWRQRLVADGILPKCGCGSGQVAILADVDETRTKTGAFAPADCAI 132  
DB 83 GGVELEVYGHYWRRELAQOKLVTSCECPENAVAVANSIQRVATAQFFITGAFPGCGI 142  
QY 133 TVHTQADTSSPDPLFNPPLKTGVCQJDNANVTDAI-LEBAGSIAIDFTGHYQTAFRELERV 191  
DB 143 PVHHPQMGCTMDPTNPVITDSDSPAFREKALQAMKEKQGMQUR-----SKLEFTM 195  
QY 192 LNFPGSNCLKREKODESCSLTQALPSBLKVADCVSLTGAVSLASMTTEIFLLQQAQM 251  
DB 196 IDYRNSPSC---KEKVCYSLEGGDTFSAGYQCGEPGVSGPLKVNLSIVDAFTIQQYEFG 251  
QY 252 P--EENGCRITDSDHOMNTLSTLHNAQFDLQRTPEVARSRAPTPLDITKTLTHHPQKQ 309  
DB 252 PDDQVANKGEIASDKMRLSKIKNGYQSLFITSVAVAQNAKPLVKYIDNALVGBGASK- 310  
QY 310 AYGVTLPTSVLFIAGHDNTLANIGALELN-WTLPGQPDNTPPGGELVEFERMRSLSDNSQ 368  
DB 311 -----AKVTLVGHDSNISILTALDPKPYQLFGQYERTPIGKLLFORWHSAGVRD 363  
QY 369 WIOGSLVFQTLQOMKDKTPISLNTPGGEVKLTLAGCEERNAGMCSLAGTQIVNEA 425  
DB 364 LMKIYVYQSTQJLNADALITQAPFORVTLALNGCPV-DIOGFCPLFTFMVINEA 419

RESULT 7  
US-09-489-039A-13501  
; Sequence 13501, Application US/09489039A  
; Patent No. 6610836  
; GENERAL INFORMATION:  
; APPLICANT: Gary Breton et. al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA  
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 2709.2004001  
; CURRENT APPLICATION NUMBER: US/09/489,039A  
; CURRENT FILING DATE: 2000-01-27  
; PRIOR APPLICATION NUMBER: US 60/117,747  
; PRIOR FILING DATE: 1999-01-29  
; NUMBER OF SEQ ID NOS: 14342  
; SEQ ID NO 13501  
; LENGTH: 522  
; TYPE: PRF  
; ORGANISM: Klebsiella pneumoniae  
US-09-489-039A-13501

Query Match 16.9%; Score 381; DB 4; Length 522;  
Best Local Similarity 26.3%; Pred. No. 2,3e-31;  
Matches 117; Conservative 73; Mismatches 209; Indels 46; Gaps 15;

QY 2 KALLIPSLILPLP-OSAPFQSEPELKSIVSVSHRGVAPKAI-QLMQDVTTPAW 59  
DB 107 QGLHLFLTACALPLALQSAAA---ADWOLEKVALSHHGIRPFAGRREAIETATGRFW 163  
QY 60 PTWPVKGLTPRGGELIAYLGHYWRQRLVADGILPKCGCGSGQVAILADVDETRTKTG 119  
DB 164 TWTHTHDEGLGHYAAVAVNKGRAQGHYRQGLL-QAGCPTASIIYVRAAPLQRTATA 222  
QY 120 EAPFAGLAPDCAITVHTQADTSSPDPLFNPPLKTGVCQJDNANVTDAIIEBAGSIAIDFTG 179  
DB 223 QALVDGAFPGCVAAHYV--SGDADPLFOTDFAATQTDPAKQLAAREKAG---DLAQ 276  
QY 180 HYQTAFRELERVIANFQSNCLKREKODESCSLTQALPSBLKVADCVSLTGAVSLASMTL 239  
DB 277 RRGQ----LAPTIQLKQAVC---QADKPCPIPT-PMOYEQSGKTTISGLSVANM 327  
QY 240 TEIFLLQQAQSNP--EPGGRITDSDHOMNTLSTLHNAQFDLQRTPEVARSRAPTPLDLI 297  
DB 328 VETLRIGSENPLSOLAWKITQARQITALLPLLTENYDITLNDVLYTAQKGSVLLNAM 387  
QY 298 KTAALPHPEQKQAYGVTLPSTVLFAGHDNTLANIGALELNMTLPG-QPDNTPGGEVL 356  
DB 388 LDGVKPEANPNVR-----LLVADHTINAVRTIMNSWQLPGVSRGNIPPGSSLV 439

QY 357 FERMRSLNSQMIQVSLVFQTLQOMKDKTPISLNTPGGEVKLT-----LAGCEERNAG 411  
DB 440 LERMRNKGGERLYLRVFOAQGLDILR-----RLQTPAQHMLROEWHOPGCRQTDVGT 494  
QY 412 MC-----SLAGTQIVNEARIPACSL 432  
DB 495 LCPFOAITALQGRIDRSSAPAVAM 519

RESULT 8  
US-09-044-718-3  
; Sequence 3, Application US/09044718  
; Patent No. 6391605  
; GENERAL INFORMATION:  
; APPLICANT: KOSTERMA, Dirk  
; APPLICANT: PASAMONTES, Luis  
; APPLICANT: TOMSCHY, Andrea  
; APPLICANT: van LOON, Adolphus  
; APPLICANT: VOGEL, Kurt  
; APPLICANT: WYSS, Markus  
; TITLE OF INVENTION: MODIFIED PHRYASES  
; FILE REFERENCE: Modified Phrases  
; CURRENT APPLICATION NUMBER: US-09/044,718  
; CURRENT FILING DATE: 1998-03-19  
; PRIOR APPLICATION NUMBER: EP 97810175.6  
; PRIOR FILING DATE: 1997-03-25  
; NUMBER OF SEQ ID NOS: 82  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 3  
; LENGTH: 439  
; TYPE: PRF  
; ORGANISM: Aspergillus fumigatus  
US-09-044-718-3

Query Match 5.6%; Score 126; DB 4; Length 439;  
Best Local Similarity 20.9%; Pred. No. 0.00017;  
Matches 102; Conservative 69; Mismatches 166; Indels 150; Gaps 26;

QY 7 PLSLILPITPQAFQSEPELKSIVSVSHRGVAPLT-----KATQIMQDVTDA--- 58  
DB 26 PFLSLDELSVSKLPK--DCRITLVQVLSRHGARYPTSSKSKYKLVTAIQANADTF 82  
QY 59 -----WPTWPVKLG--ELTPRGGELIAYLG--HYWRQRLVADGILPKCGCGSGQVAIL 108  
DB 83 KGFAPFLKTYNNYTLGADDLTPRGGELIAYLGHYWRQRLVADGILPKCGCGSGQVAIL 132  
QY 109 ADVDETRTKTGAFAPAGL-----APDCAITVHTQADTSSPDPLFNPPLKTGV 154  
DB 133 AGSDRVIASGEKFIQFOQAKLADPGATNRAAPALSVII-DESETFN-----NTLDHGV 186  
QY 155 C-OLDNANVTDALEBAGSIAIDFTGHYQTAFRELERVIANFQSNCLKREKODESCSLT 213  
DB 187 CTKEFASQGDGV-----ANFTALFPADIR-----AAAEKH----- 218  
QY 214 QALPSELKVSADCVSLTGAVSLASMTTEIFLLQQAQMEPQMGRTDSDHOMNTLSTL-- 271  
DB 219 --LPVTLTDEBDVYSLMDKSPDTV-----ARTSDASQLSPFQGLPT 258  
QY 272 HN--AQPDILQ-----TPE-VARSRAPTPLDLIKI--ALTPRP 305  
DB 259 HNMWKXNYNLQSLGKYYGYGAGNPLGPAQIGFTMELIARLRSVPQDHTSTNLTIVSNP 318  
QY 306 POKQAYGVTLPSTVFLIA--GHDTNLANIGALELNMTLPQGPDPNTPPGGELVFERMRSL 363  
DB 319 -----ATPPLNATMYVFPESHNSVSLFPAL-----GLYNGTEPLSTRSVSAXEL 364  
QY 364 SD-NSQWT---QVSLVFQTLQOMKDKTPISLNTPGGEVKLTLAGCEERNAGMCSLAGT 419  
DB 365 DGYSASVVFPGARAVFETMQCKSEKPL-VRALINDRVVPLHGCDV-DKLGRCKLNDV 422  
QY 420 QIVNEAR 426  
DB 423 KGLSMAR 429

RESULT 9  
US-09-684-855-106  
; Sequence 106, Application US/09684855  
; Patent No. 6599735  
; GENERAL INFORMATION:  
; APPLICANT: F. Hoffmann-La Roche AG  
; TITLE OF INVENTION: CONTINUOUS FERMENTATION PROCESS  
; FILE REFERENCE: C38435/11692  
; CURRENT APPLICATION NUMBER: US/09/684,855  
; PRIOR FILING DATE: 2000-10-06  
; PRIOR APPLICATION NUMBER: EP 00121663.9  
; PRIOR FILING DATE: 2000-10-04  
; PRIOR APPLICATION NUMBER: EP 99120289.6  
; PRIOR FILING DATE: 1999-10-11  
; NUMBER OF SEQ ID NOS: 169  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 106  
; LENGTH: 440  
; TYPE: PRF  
; ORGANISM: A. fumigatus 13073  
US-09-684-855-106

Query Match 5.6%; Score 126; DB 4; Length 440;  
Best Local Similarity 20.9%; Pred. No. 0.00017;  
Matches 102; Conservative 69; Mismatches 166; Indels 150; Gaps 26;

QY 7 PFLSLIPLTPGSAFAQSEBELKLESVIVSRHGVRAPT-----KATQLMQDVTTPDA--- 58  
DB 27 PFLSLEDELISVSSKLPK---DCRITLVQVLSRHGARYPTSSKSKYKCLVTAIQANATDF 83  
QY 59 -----WPTWPKVG--ELTPRGGEIAYIG--HYWRQRLVADGLPKGCGPQSGQVAII 108  
DB 84 KGRKPAFLKTYNTLTGADDLTPFGHQQLVNSGIRFYQRYKALASVVF-----FIR 133  
QY 109 ADVDERTRKTGEAFPAAGL-----APDCATVHTQADTSSPDPLFNPLKGTGV 154  
DB 134 ASGSDRIYASGEKFTFEGFOQAKLADPGATNRAAPAIISVII--PESSEFN-----NTLDHGV 187  
QY 155 C-QLDNANVTDAILERAGGSIADFTGHYQTAFFELERVLNFPQSNCLKREKDESCSLT 213  
DB 188 CTKEFAAQQLDEV-----AANFTALFAPDIR-----ARAEKH----- 219  
QY 214 QALPSELKVASDVCVSLTGAVSLASMLTEIFLLQQAQMPERPWGRTDTSNQNTLLSL-- 271  
DB 220 --LPGVTLTDEVDVSLMDMCSFDTV-----ARTSDASQLSPFQQLFT 259  
QY 272 HN--AQFDLQOR-----TPE-VASRATPLLDLTKT--ALTHP 305  
DB 260 HNEWKXNYVLSQGLKYYGAGNPLGPAQIGFTNELIALRTSPVQDHTSTNSTLVSNP 319  
QY 306 POKRAYVTLPTSLVFLA--GHDNTLANLGALEIMNTLPGQPDNTPPGSELVFERMRRL 363  
DB 320 -----ATFPLNATWYVDFSHDMSWVSIFPAL-----GLYNGTEPLSRSTSASAKEL 365  
QY 364 SD-NSQWIT---QVSLVFQTLQQRMDKTPSLNTPRGVSKTLTAGCERNAQMGCSLAGFT 419  
DB 366 DGYASWVVPFGARAYETWQCKSEKPEL-VRALINDRVVPLHGDV-DLGRCKLNDPV 423  
QY 420 QIVNEAR 426  
DB 424 KGLSWAR 430

RESULT 10  
US-09-684-855-128  
; Sequence 128, Application US/09684855  
; Patent No. 6599735  
; GENERAL INFORMATION:  
; APPLICANT: F. Hoffmann-La Roche AG  
; TITLE OF INVENTION: CONTINUOUS FERMENTATION PROCESS  
; FILE REFERENCE: C38435/11692

CURRENT APPLICATION NUMBER: US/09/684,855  
; CURRENT FILING DATE: 2000-10-06  
; PRIOR APPLICATION NUMBER: EP 00121663.9  
; PRIOR FILING DATE: 2000-10-04  
; PRIOR APPLICATION NUMBER: EP 99120289.6  
; PRIOR FILING DATE: 1999-10-11  
; NUMBER OF SEQ ID NOS: 169  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 128  
; LENGTH: 440  
; TYPE: PRF  
; ORGANISM: A. fumigatus 13073  
US-09-684-855-128

Query Match 5.6%; Score 126; DB 4; Length 440;  
Best Local Similarity 20.9%; Pred. No. 0.00017;  
Matches 102; Conservative 69; Mismatches 166; Indels 150; Gaps 26;

QY 7 PFLSLIPLTPGSAFAQSEBELKLESVIVSRHGVRAPT-----KATQLMQDVTTPDA--- 58  
DB 27 PFLSLEDELISVSSKLPK---DCRITLVQVLSRHGARYPTSSKSKYKCLVTAIQANATDF 83  
QY 59 -----WPTWPKVG--ELTPRGGEIAYIG--HYWRQRLVADGLPKGCGPQSGQVAII 108  
DB 84 KGRKPAFLKTYNTLTGADDLTPFGHQQLVNSGIRFYQRYKALASVVF-----FIR 133  
QY 109 ADVDERTRKTGEAFPAAGL-----APDCATVHTQADTSSPDPLFNPLKGTGV 154  
DB 134 ASGSDRIYASGEKFTFEGFOQAKLADPGATNRAAPAIISVII--PESSEFN-----NTLDHGV 187  
QY 155 C-QLDNANVTDAILERAGGSIADFTGHYQTAFFELERVLNFPQSNCLKREKDESCSLT 213  
DB 188 CTKEFAAQQLDEV-----AANFTALFAPDIR-----ARAEKH----- 219  
QY 214 QALPSELKVASDVCVSLTGAVSLASMLTEIFLLQQAQMPERPWGRTDTSNQNTLLSL-- 271  
DB 220 --LPGVTLTDEVDVSLMDMCSFDTV-----ARTSDASQLSPFQQLFT 259  
QY 272 HN--AQFDLQOR-----TPE-VASRATPLLDLTKT--ALTHP 305  
DB 260 HNEWKXNYVLSQGLKYYGAGNPLGPAQIGFTNELIALRTSPVQDHTSTNSTLVSNP 319  
QY 306 POKRAYVTLPTSLVFLA--GHDNTLANLGALEIMNTLPGQPDNTPPGSELVFERMRRL 363  
DB 320 -----ATFPLNATWYVDFSHDMSWVSIFPAL-----GLYNGTEPLSRSTSASAKEL 365  
QY 364 SD-NSQWIT---QVSLVFQTLQQRMDKTPSLNTPRGVSKTLTAGCERNAQMGCSLAGFT 419  
DB 366 DGYASWVVPFGARAYETWQCKSEKPEL-VRALINDRVVPLHGDV-DLGRCKLNDPV 423  
QY 420 QIVNEAR 426  
DB 424 KGLSWAR 430

RESULT 11  
US-09-684-855-151  
; Sequence 151, Application US/09684855  
; Patent No. 6599735  
; GENERAL INFORMATION:  
; APPLICANT: F. Hoffmann-La Roche AG  
; TITLE OF INVENTION: CONTINUOUS FERMENTATION PROCESS  
; FILE REFERENCE: C38435/11692  
; CURRENT APPLICATION NUMBER: US/09/684,855  
; PRIOR FILING DATE: 2000-10-06  
; PRIOR APPLICATION NUMBER: EP 00121663.9  
; PRIOR FILING DATE: 2000-10-04  
; PRIOR APPLICATION NUMBER: EP 99120289.6  
; PRIOR FILING DATE: 1999-10-11  
; NUMBER OF SEQ ID NOS: 169  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 151  
; LENGTH: 440

Tue May 4 07:05:29 2004

us-09-866-379d-10.rai

Page 6

TYPE: PRT  
ORGANISM: A. fumigatus 32722  
US-09-684-855-151

Query Match 5.6%; Score 126; DB 4; Length 440;  
Best Local Similarity 20.9%; Pred. No. 0.00017;  
Matches 102; Conservative 69; Mismatches 166; Indels 150; Gaps 26;

QY 7 PFLSLIPLTPQSAFAQSEBELKESVIVSRHGVAPF-----KATQIMQDVTBDA--- 58  
DB 27 PFPSEBELSVSSKPKR---DCRITLVQVLSRHGARYPTSSKSKYKLVATIAQANADF 83  
QY 59 -----WPTWPKVG--ELTPRGELIAYLG--HYWRQLVADGILLPKGCGQSQVAIL 108  
DB 84 KGFAPLKYNTYTLGADDLTPFGEQLVNSGIKFYQRYKALARSVP-----FIR 133  
QY 109 ADVDERTRKTGEAFAGL-----APDCATVHTQADTSSPDPLFNLKXGV 154  
DB 134 ASGSDRVIASGEKFTIEGFOQAKLADPGATNRAAPALSVII-PESETFN-----NTLDHGV 187  
QY 155 C-OLDNANTDAILERAGSISADFTGHYQTAFFELERVLNFPQSNICLRKQDESCSLT 213  
DB 188 CTRFASQLGDEV-----ANFTALFAPDIR-----ARAERH----- 219  
QY 214 QALPSELKVSADCVSLTGAVSLASMLTEIFLLQQAQMPGPGWGRITDSHQNMTLLSL-- 271  
DB 220 --LPGVTLTDEVDVSLMDKSPDTV-----ARTSDASQLSPPCQLFT 259  
QY 272 HN--AQFDLLQR-----TPE-VARSRATPLDLIKT--ALTPHP 305  
DB 260 HNEWKKNYVLSIGKRYGYGAGNPLGPAQGIPTNELIARLTRSPVQDHTSTNSTLVSNP 319  
QY 306 PQKQAVGVTLPTSVLFIA--GHDTNLANIAGALELAWTLPGQPDNTPPGGELVFERWRRL 363  
DB 320 -----ATFPLNATMYVDFSHNSWVSIFPAL-----GLYNGTEPLSRTSVESAKEL 365  
QY 364 SD-NSQMI---QVSLVFQTLQQRDKTPLSLNTPPGEVKITLAGEERNAQMGCSLAGFT 419  
DB 366 DGYSASNVVPFGARAYETMQCKSEKPEL-VRALINDRVVPLHGCIV-DKLGRCXKLANDPV 423  
QY 420 QIVNEAR 426  
DB 424 KGLSMAR 430

RESULT 12  
US-09-044-718-12  
Sequence 12, Application US/09044718  
Patent No. 6391605

GENERAL INFORMATION:  
APPLICANT: KOSTREMA, Dirk  
APPLICANT: PASAMONTES, Luis  
APPLICANT: TOMSCHY, Andrea  
APPLICANT: van LOON, Adolphus  
APPLICANT: VOGEL, Kurt  
TITLE OF INVENTION: MODIFIED PHYTASES  
FILE REFERENCE: Modified Phytases  
CURRENT APPLICATION NUMBER: US/09/044,718  
CURRENT FILING DATE: 1998-03-19  
PRIOR APPLICATION NUMBER: EP 97810175.6  
PRIOR FILING DATE: 1997-03-25  
NUMBER OF SEQ ID NOS: 82  
SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 12  
LENGTH: 449  
TYPE: PRT  
ORGANISM: Aspergillus fumigatus  
US-09-044-718-12

Query Match 5.6%; Score 126; DB 4; Length 449;  
Best Local Similarity 20.9%; Pred. No. 0.00018;  
Matches 102; Conservative 69; Mismatches 166; Indels 150; Gaps 26;

QY 7 PFLSLIPLTPQSAFAQSEBELKESVIVSRHGVAPF-----KATQIMQDVTBDA--- 58  
DB 36 PFPSEBELSVSSKPKR---DCRITLVQVLSRHGARYPTSSKSKYKLVATIAQANADF 92  
QY 59 -----WPTWPKVG--ELTPRGELIAYLG--HYWRQLVADGILLPKGCGQSQVAIL 108  
DB 93 KGFAPLKYNTYTLGADDLTPFGEQLVNSGIKFYQRYKALARSVP-----FIR 142  
QY 109 ADVDERTRKTGEAFAGL-----APDCATVHTQADTSSPDPLFNLKXGV 154  
DB 143 ASGSDRVIASGEKFTIEGFOQAKLADPGATNRAAPALSVII-PESETFN-----NTLDHGV 196  
QY 155 C-OLDNANTDAILERAGSISADFTGHYQTAFFELERVLNFPQSNICLRKQDESCSLT 213  
DB 197 CTRFASQLGDEV-----ANFTALFAPDIR-----ARAERH----- 228  
QY 214 QALPSELKVSADCVSLTGAVSLASMLTEIFLLQQAQMPGPGWGRITDSHQNMTLLSL-- 271  
DB 229 --LPGVTLTDEVDVSLMDKSPDTV-----ARTSDASQLSPPCQLFT 268  
QY 272 HN--AQFDLLQR-----TPE-VARSRATPLDLIKT--ALTPHP 305  
DB 269 HNEWKKNYVLSIGKRYGYGAGNPLGPAQGIPTNELIARLTRSPVQDHTSTNSTLVSNP 328  
QY 306 PQKQAVGVTLPTSVLFIA--GHDTNLANIAGALELAWTLPGQPDNTPPGGELVFERWRRL 363  
DB 329 -----ATFPLNATMYVDFSHNSWVSIFPAL-----GLYNGTEPLSRTSVESAKEL 374  
QY 364 SD-NSQMI---QVSLVFQTLQQRDKTPLSLNTPPGEVKITLAGEERNAQMGCSLAGFT 419  
DB 375 DGYSASNVVPFGARAYETMQCKSEKPEL-VRALINDRVVPLHGCIV-DKLGRCXKLANDPV 432  
QY 420 QIVNEAR 426  
DB 433 KGLSMAR 439

RESULT 13  
US-08-868-435-33  
Sequence 33, Application US/08868435  
Patent No. 6291221

GENERAL INFORMATION:  
APPLICANT: Van Loon, Adolphus  
APPLICANT: Mitchell, David  
TITLE OF INVENTION: POLYPEPTIDES WITH PHYTASE ACTIVITY  
NUMBER OF SEQUENCES: 35  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hoffmann-La Roche Inc.  
STREET: 340 Kingeland Street  
CITY: Nutley  
STATE: New Jersey  
COUNTRY: United States of America  
ZIP: 07110  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/868,435  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/744,231  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Kase, Alan P  
REGISTRATION NUMBER: 32142  
REFERENCE/DOCKET NUMBER: Case Docket 9339  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (201) 235-4205  
TELEFAX: (201) 235-2363

INFORMATION FOR SEQ ID NO: 33:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 465 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: 104  
OTHER INFORMATION: /note="potential N-glycosylation site"  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: 119  
OTHER INFORMATION: /note="potential N-glycosylation site"  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: 205  
OTHER INFORMATION: /note="potential N-glycosylation site"  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: 228  
OTHER INFORMATION: /note="potential N-glycosylation site"  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: 337  
OTHER INFORMATION: /note="potential N-glycosylation site"  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: 374  
OTHER INFORMATION: /note="potential N-glycosylation site"  
US-08-866-435-33

Query Match 5.6%; Score 126; DB 3; Length 465;  
Best Local Similarity 20.9%; Pred. No. 0.00019;  
Matches 102; Conservative 69; Mismatches 166; Indels 150; Gaps 26;

7 PLSLLIPLPQSAFQSEPELKSIVIVSRHGVRAPI-----KATQIMQDVTPEA--- 58  
52 PPSLDELDELSSVSKPK--DRLITLVQLSRHGRARYPTSSSKYKKLVLVAIQANADF 108  
59 -----WPTPVKLG--ELTPRGELIAYLG--HYRQQLVADGLLEPKCGQSGVAII 108  
109 KGFPAFLKTYNTLTGADLTPEEQQLVNSGIRYQRYALARSVP-----FIR 158  
109 ADVDERTRTGAFAPAGL-----APDCATVHQADTSSPDLFNLKTV 154  
159 ASGSDRVIASGEKFTBGFQQAALADPGATMRAAPALSVII-PESETFN-----NTLDHGV 212  
155 C-QLDNNANTDAILERRAGSIAFTGHYQTAFFRELERVLNFPQSNLCIKREKODESCSLT 213  
213 CTKFEASQIGDEV-----ANFTALFAPDIR-----ARAEGK----- 244  
214 QALPEELKISADCVSITGAVSLASMLTEFLQQAQMPGEMGRITLTHONTLLSL-- 271  
245 --LPGVTLTDEBVVSLMDVCSFDIV-----ARTSDSQSLSPCCQLFT 284  
272 HN--AQFDLLQR-----TBE-VARSRATPLDLIKT--ALTRHP 305  
285 HHEWKKYVYLQSLGKYYGAGNPLGAPAGIGFTVHELIARLTRSPVDHSTNSTLVSNP 344  
306 POKQAVGVLTFTSVLFIA--GHDITNANIGALELNTWITPQGPDMTPRGDELVEFERMRL 363  
345 -----ATFPFNATVYDFSHNSVVSIFAL-----GLYNGTEPLSRTVSBAHEL 390  
364 SD-NSQMI-----QVSLVFQTLQQRDRKTPSLNTPPEGVALLTAGSEERNAQMCSLAGFT 419  
391 DGSASAVVVPFGRAAFETMCKSEKPL-VRALINDRVVPLHGCV-DKGRCLNDLV 448  
420 QIVNEAR 426  
449 KGLSMAR 455

RESULT 14  
US-08-744-231-33  
Sequence 33; Application US/08744231  
Patent No. 6358722  
GENERAL INFORMATION:  
APPLICANT: Van Loon, Adolphus  
TITLE OF INVENTION: POLYPEPTIDES WITH PHYTASE ACTIVITY  
NUMBER OF SEQUENCES: 35  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hoffmann-La Roche Inc.  
STREET: 340 Kingsland Street  
CITY: Nutley  
STATE: New Jersey  
COUNTRY: United States of America  
ZIP: 07110

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Releasee #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/744,231  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/424,757  
FILING DATE: 18-APR-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Kaas, Alan P  
REGISTRATION NUMBER: 32142  
REFERENCE/DOCKET NUMBER: Case Docket 9339  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (201) 235-4205  
TELEFAX: (201) 235-2363

INFORMATION FOR SEQ ID NO: 33:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 465 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: 104  
OTHER INFORMATION: /note="potential N-glycosylation site"  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: 119  
OTHER INFORMATION: /note="potential N-glycosylation site"  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: 205  
OTHER INFORMATION: /note="potential N-glycosylation site"  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: 228  
OTHER INFORMATION: /note="potential N-glycosylation site"  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: 337  
OTHER INFORMATION: /note="potential N-glycosylation site"  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: 374  
OTHER INFORMATION: /note="potential N-glycosylation site"  
US-08-744-231-33

Query Match 5.6%; Score 126; DB 4; Length 465;  
Best Local Similarity 20.9%; Pred. No. 0.00019;  
Matches 102; Conservative 69; Mismatches 166; Indels 150; Gaps 26;

7 PLSLLIPLPQSAFQSEPELKSIVIVSRHGVRAPI-----KATQIMQDVTPEA--- 58  
52 PPSLDELDELSSVSKPK--DRLITLVQLSRHGRARYPTSSSKYKKLVLVAIQANADF 108  
59 -----WPTPVKLG--ELTPRGELIAYLG--HYRQQLVADGLLEPKCGQSGVAII 108  
109 KGFPAFLKTYNTLTGADLTPEEQQLVNSGIRYQRYALARSVP-----FIR 158  
109 ADVDERTRTGAFAPAGL-----APDCATVHQADTSSPDLFNLKTV 154  
159 ASGSDRVIASGEKFTBGFQQAALADPGATMRAAPALSVII-PESETFN-----NTLDHGV 212  
155 C-QLDNNANTDAILERRAGSIAFTGHYQTAFFRELERVLNFPQSNLCIKREKODESCSLT 213  
213 CTKFEASQIGDEV-----ANFTALFAPDIR-----ARAEGK----- 244  
214 QALPEELKISADCVSITGAVSLASMLTEFLQQAQMPGEMGRITLTHONTLLSL-- 271  
245 --LPGVTLTDEBVVSLMDVCSFDIV-----ARTSDSQSLSPCCQLFT 284  
272 HN--AQFDLLQR-----TBE-VARSRATPLDLIKT--ALTRHP 305  
285 HHEWKKYVYLQSLGKYYGAGNPLGAPAGIGFTVHELIARLTRSPVDHSTNSTLVSNP 344  
306 POKQAVGVLTFTSVLFIA--GHDITNANIGALELNTWITPQGPDMTPRGDELVEFERMRL 363  
345 -----ATFPFNATVYDFSHNSVVSIFAL-----GLYNGTEPLSRTVSBAHEL 390  
364 SD-NSQMI-----QVSLVFQTLQQRDRKTPSLNTPPEGVALLTAGSEERNAQMCSLAGFT 419  
391 DGSASAVVVPFGRAAFETMCKSEKPL-VRALINDRVVPLHGCV-DKGRCLNDLV 448  
420 QIVNEAR 426  
449 KGLSMAR 455

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Db      52 PFFSLEDELVSXSKLPK---DCRITLVQVLSRHGARVPTSSKSKYKLVTAIAQANATDF 108
Qy      59 -----WPTWPKVLG--ELTPRGELIAYIG--HYRQRLVADGLLPKGCCPGSGVAILI 108
Db      109 KGRFAFLKTYNTLTGADDLTPFGBQQLVNSGIKFYQRYKALARSVP-----FIR 158
Qy      109 ADVDERTRKTGEAFPAAGL-----APDCATVHTQADTSSPDPLEFPLKTYV 154
Db      159 ASGSDRVIASGEKTEIEFPOAKLADPGATNRAAPALSVII--PSEFTN-----NTLDHGV 212
Qy      155 C-OLDNNAVTDALIERAGGSIADFTGHYQTAFRELEVLNFPQSNLCREKODESCSLT 213
Db      213 CTKEFASQLGDEV-----AANFTALFAPDIR-----ARAEKH----- 244
Qy      214 QALPSELKVSADCVSLTGAVSLASMLTEIFLLQAQGMPEPGWRITDSHQMTLSL-- 271
Db      245 --LPGVTLTDEDVSLMDMCSFDTV-----ARTSDAQSLSPFQCLFT 284
Qy      272 HN--AQEDLLQR-----TPE-VASRATPLIDLKT--ALTEHP 305
Db      285 HNEWKXVYLSGLKRYGYGAGNPLGPAQIGFTNELIARITRSPVODHTSTNSTLVSNP 344
Qy      306 POKQAVGTLPTSVLFLA--GHDTNLANLGALFLNMTLPQOPNTPPGSELVERWRRL 363
Db      345 -----ATFPLNATMYVDFSHDMSWSIFPAL-----GLYNGTEPLRTSVESAKEL 390
Qy      364 SD-NSQMT---QVSLVFQTLQOMDKTPLSLNTPPGEVKLTLAGCEERNAGMCSLAGFT 419
Db      391 DGYSASWVVPFGARAYFETMCKSEKEPL--VRALINRVVPLHGCYV-DKLGRCXKLNDFV 448
Qy      420 QIVNEAR 426
Db      449 KGLSWAR 455

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## RESULT 15

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US-09-044-718-78
; Sequence 78, Application US/09044718
; Patent No. 6391605
; GENERAL INFORMATION:
; APPLICANT: KOSTREMA, Dirk
; APPLICANT: PASAMONTES, Luis
; APPLICANT: TOMSCHY, Andrea
; APPLICANT: van LOON, Adolphus
; APPLICANT: VOGEL, Kurt
; APPLICANT: WYSS, Markus
; TITLE OF INVENTION: MODIFIED PHYTASES
; FILE REFERENCE: Modified Phytases
; CURRENT APPLICATION NUMBER: US/09/044,718
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: EP 97810175.6
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 78
; LENGTH: 465
; TYPE: PRT
; ORGANISM: Aspergillus fumigatus
US-09-044-718-78

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Query Match      5.6%; Score 126; DB 4; Length 465;
Best Local Similarity 20.9%; Pred. No. 0.00019;
Matches 102; Conservative 69; Mismatches 166; Indels 150; Gaps 26;

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Qy      59 -----WPTWPKVLG--ELTPRGELIAYIG--HYRQRLVADGLLPKGCCPGSGVAILI 108
Db      109 KGRFAFLKTYNTLTGADDLTPFGBQQLVNSGIKFYQRYKALARSVP-----FIR 158
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Qy      420 QIVNEAR 426
Db      449 KGLSWAR 455

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Search completed: May 2, 2004, 00:56:56
Job time : 50 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 2, 2004, 00:51:12 ; Search time 86 Seconds  
(without alignments)

1392.394 Million cell updates/sec

Title: US-09-866-379D-10

Perfect score: 2258  
Sequence: 1 MKALIPFLSLPLTPQSA.....CSLAGTQIVNEARIPACSL 432

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1138120 seqs, 277189581 residues

Total number of hits satisfying chosen parameters: 1138120

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:\*

- 1: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep.\*
- 2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep.\*
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- 13: /cgn2\_6/ptodata/2/pubpaa/US10B\_PUBCOMB.pep.\*
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- 17: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*
- 18: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2258	100.0	436	14	US-10-156-660-2
2	2228	98.7	430	9	US-09-866-379-10
3	2182	96.6	432	9	US-09-866-379-8
4	2182	96.6	432	12	US-10-282-122A-43351
5	2182	96.6	432	14	US-10-156-660-4
6	2171	96.1	440	9	US-09-777-566A-2
7	2171	96.1	440	9	US-09-866-379-2
8	2171	96.1	440	14	US-10-034-985-2
9	2171	96.1	440	15	US-10-430-356-2
10	2157	95.5	412	14	US-10-334-672-1
11	2157	95.5	412	14	US-10-334-671-1
12	2153	95.3	410	14	US-10-021-723A-13
13	2153	95.3	410	14	US-10-021-723A-15
14	2147	95.1	432	15	US-10-284-962-3
15	2147	95.1	432	15	US-10-284-962-14

16	2147	95.1	433	14	US-10-266-041-1	Sequence 1, Appli
17	2144	95.0	432	15	US-10-284-962-5	Sequence 2, Appli
18	2112	93.5	432	14	US-10-021-723A-16	Sequence 16, Appli
19	976.5	43.2	441	14	US-10-021-723A-12	Sequence 12, Appli
20	959.5	42.5	441	12	US-10-282-122A-77792	Sequence 77792, A
21	951.5	42.1	441	14	US-10-021-723A-2	Sequence 2, Appli
22	948.5	42.0	441	14	US-10-021-723A-4	Sequence 4, Appli
23	782	34.6	416	14	US-10-021-723A-10	Sequence 10, Appli
24	627.5	27.8	318	14	US-10-021-723A-14	Sequence 8, Appli
25	475.5	21.1	409	14	US-10-021-723A-8	Sequence 6, Appli
26	462.5	20.5	421	14	US-10-021-723A-6	Sequence 44, Appli
27	197	8.7	426	12	US-10-257-174-44	Sequence 6, Appli
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29	126	5.6	439	14	US-10-063-848-3	Sequence 3, Appli
30	126	5.6	440	12	US-10-442-538-106	Sequence 106, App
31	126	5.6	440	12	US-10-442-538-128	Sequence 128, App
32	126	5.6	440	12	US-10-442-538-151	Sequence 151, App
33	126	5.6	449	14	US-10-062-848-12	Sequence 12, Appli
34	126	5.6	465	13	US-10-083-452-8	Sequence 8, Appli
35	126	5.6	465	14	US-10-062-848-78	Sequence 78, Appli
36	126	5.6	465	14	US-10-229-358-6	Sequence 6, Appli
37	125	5.5	474	14	US-10-213-980-24	Sequence 24, Appli
38	125	5.5	440	12	US-10-442-538-107	Sequence 107, App
39	125	5.5	440	12	US-10-442-538-129	Sequence 129, App
40	125	5.5	440	12	US-10-442-538-152	Sequence 152, App
41	124	5.5	467	12	US-10-442-538-165	Sequence 165, App
42	122.5	5.2	99	12	US-10-282-132A-59099	Sequence 59099, A
43	118	5.2	440	12	US-10-442-538-108	Sequence 108, App
44	118	5.2	440	12	US-10-442-538-130	Sequence 130, App
45	118	5.2	440	12	US-10-442-538-153	Sequence 153, App

#### ALIGNMENTS

RESULT 1  
US-10-156-660-2  
Sequence 2, Application US/10156660  
Publication No. US20030103958A1  
GENERAL INFORMATION:  
APPLICANT: Short, Jay M.  
APPLICANT: Kretz, Keith  
APPLICANT: Gray, Kevin A.  
APPLICANT: Barton, Nelson R.  
APPLICANT: Garrett, James B.  
APPLICANT: O'Donoghue, Eileen  
APPLICANT: Mathur, Eric J.  
TITLE OR INVENTION: PHYTASES, NUCLEIC ACIDS ENCODING THEM  
TITLE OR INVENTION: AND METHODS FOR MAKING AND USING THEM  
FILE REFERENCE: 09010-029007  
CURRENT APPLICATION NUMBER: US/10/156,660  
CURRENT FILING DATE: 2002-10-01  
PRIOR APPLICATION NUMBER: US 09/866,379  
PRIOR FILING DATE: 2001-05-24  
PRIOR APPLICATION NUMBER: US 09/580,515  
PRIOR FILING DATE: 2000-05-25  
PRIOR APPLICATION NUMBER: US 09/318,528  
PRIOR FILING DATE: 1999-05-25  
PRIOR APPLICATION NUMBER: US 09/291,931  
PRIOR FILING DATE: 1999-04-13  
PRIOR APPLICATION NUMBER: US 09/259,214  
PRIOR FILING DATE: 1999-03-01  
PRIOR APPLICATION NUMBER: US 08/910,798  
PRIOR FILING DATE: 1997-08-13  
NUMBER OF SEQ ID NOS: 4  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 2  
LENGTH: 436  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: modified phytase enzyme  
US-10-156-660-2

Query Match 100.0%; Score 2258; DB 14; Length 436;  
 Best Local Similarity 100.0%; Pred. No. 3,8e-208;  
 Matches 432; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 301 LTPHPQKQAYGVTLPTSVLFIAGHDNTLANIGALEINMTLPQCPDNTPPGSELVFERW 360  
 DB 301 LTPHPQKQAYGVTLPTSVLFIAGHDNTLANIGALEINMTLPQCPDNTPPGSELVFERW 360

QY 361 RLSDNSQWITQVSLVFQTLQQRDKTPLSLNTPGGEVYLTLAGGERNAQMGSLAGFTQ 420  
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QY 421 IVNEARIPACSL 432  
 DB 421 IVNEARIPACSL 432

RESULT 2  
 US-09-866-379-10  
 ; Sequence 10, Application US/09866379  
 ; Patent No. US20020136754A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: DIVERSA CORPORATION  
 ; APPLICANT: SHORT, Jay  
 ; APPLICANT: KREITZ, Keith  
 ; APPLICANT: GRAY, Kevin  
 ; APPLICANT: BARTON, Nelson  
 ; APPLICANT: GARRETT, James  
 ; APPLICANT: O'DONOGHUE, Eileen  
 ; TITLE OF INVENTION: RECOMBINANT BACTERIAL PHYTASES AND USES THEREOF  
 ; FILE REFERENCE: DIVER1370-7  
 ; CURRENT APPLICATION NUMBER: US/09/866,379  
 ; PRIOR FILING DATE: 2001-05-24  
 ; PRIOR APPLICATION NUMBER: US 09/580,515  
 ; PRIOR FILING DATE: 2000-05-25  
 ; PRIOR APPLICATION NUMBER: US 09/318,528  
 ; PRIOR FILING DATE: 1999-05-25  
 ; PRIOR APPLICATION NUMBER: US 09/291,931  
 ; PRIOR FILING DATE: 1999-04-13  
 ; PRIOR APPLICATION NUMBER: US 09/259,214  
 ; PRIOR FILING DATE: 1999-03-01  
 ; PRIOR APPLICATION NUMBER: US 08/910,798  
 ; PRIOR FILING DATE: 1997-08-13  
 ; NUMBER OF SEQ ID NOS: 10  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 10  
 ; LENGTH: 430  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Modified phybase  
 ; US-09-866-379-10

Query Match 98.7%; Score 2228; DB 9; Length 430;  
 Best Local Similarity 99.5%; Pred. No. 2.8e-205;  
 Matches 430; Conservative 0; Mismatches 0; Indels 2; Gaps 2;

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 DB 1 MKAILPFLSLILPLTPQSAFAQSEPELKLESVIVSRHGVRAPTATQTMQVTPDAMP 60

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 DB 241 EIFLLQQAQGMPEPQMGRIITDSHQWNTLLSIHNAQFDLQRTPEVARSRAATPLLDILKTA 298

QY 301 LTPHPQKQAYGVTLPTSVLFIAGHDNTLANIGALEINMTLPQCPDNTPPGSELVFERW 360  
 DB 299 LTPHPQKQAYGVTLPTSVLFIAGHDNTLANIGALEINMTLPQCPDNTPPGSELVFERW 358

QY 361 RLSDNSQWITQVSLVFQTLQQRDKTPLSLNTPGGEVYLTLAGGERNAQMGSLAGFTQ 420  
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QY 421 IVNEARIPACSL 432  
 DB 419 IVNEARIPACSL 430

RESULT 3  
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 ; Sequence 8, Application US/09866379  
 ; Patent No. US20020136754A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: DIVERSA CORPORATION  
 ; APPLICANT: SHORT, Jay  
 ; APPLICANT: KREITZ, Keith  
 ; APPLICANT: GRAY, Kevin  
 ; APPLICANT: BARTON, Nelson  
 ; APPLICANT: GARRETT, James  
 ; APPLICANT: O'DONOGHUE, Eileen  
 ; TITLE OF INVENTION: RECOMBINANT BACTERIAL PHYTASES AND USES THEREOF  
 ; FILE REFERENCE: DIVER1370-7  
 ; CURRENT APPLICATION NUMBER: US/09/866,379  
 ; PRIOR FILING DATE: 2001-05-24  
 ; PRIOR APPLICATION NUMBER: US 09/580,515  
 ; PRIOR FILING DATE: 2000-05-25  
 ; PRIOR APPLICATION NUMBER: US 09/318,528  
 ; PRIOR FILING DATE: 1999-05-25  
 ; PRIOR APPLICATION NUMBER: US 09/291,931  
 ; PRIOR FILING DATE: 1999-04-13  
 ; PRIOR APPLICATION NUMBER: US 09/259,214  
 ; PRIOR FILING DATE: 1999-03-01  
 ; PRIOR APPLICATION NUMBER: US 08/910,798  
 ; PRIOR FILING DATE: 1997-08-13  
 ; NUMBER OF SEQ ID NOS: 10  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 8  
 ; LENGTH: 432  
 ; TYPE: PRT  
 ; ORGANISM: Escherichia coli  
 ; US-09-866-379-8

Query Match 96.6%; Score 2182; DB 9; Length 432;

Best Local Similarity 98.1%; Pred. No. 7.6e-201;  
Matches 424; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

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Db 181 YOTAFRELERVLPQSNLCLKREKODESCSLTQALPSELKVSADCVSLTGAVSLASMLT 240  
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241 EIFLLQQAQMPGPGNGRITDSHQWNTLLSLHNAQFLLQRTPEVASRATPLDLIKTA 300

Db 241 EIFLLQQAQMPGPGNGRITDSHQWNTLLSLHNAQFLLQRTPEVASRATPLDLIKTA 300  
241 EIFLLQQAQMPGPGNGRITDSHQWNTLLSLHNAQFLLQRTPEVASRATPLDLIKTA 300

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Db 301 LTPHPQKQAYGVLPTSVLFIAGHDNTLANLGGALBLNMTLPGQPDNTPPGSELVFERW 360  
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QY 361 RRLSDNSQWIVSVFQTLQCMRDKTPSLNTPGEXKLTLAGCEERNAQMGSLAGFTQ 420  
361 RRLSDNSQWIVSVFQTLQCMRDKTPSLNTPGEXKLTLAGCEERNAQMGSLAGFTQ 420

Db 361 RRLSDNSQWIVSVFQTLQCMRDKTPSLNTPGEXKLTLAGCEERNAQMGSLAGFTQ 420  
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QY 421 IVNEARIPACSL 432  
421 IVNEARIPACSL 432

Db 421 IVNEARIPACSL 432  
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RESULT 4  
US-10-282-122A-43351  
Sequence 43351, Application US/10282122A  
Publication No. US20040029129A1  
GENERAL INFORMATION:  
APPLICANT: Wang, Liangsu  
APPLICANT: Zamudio, Carlos  
APPLICANT: Malone, Cheryl  
APPLICANT: Haselbeck, Robert  
APPLICANT: Ohlsen, Kari  
APPLICANT: Zykand, Judith  
APPLICANT: Wall, Daniel  
APPLICANT: Trawick, John  
APPLICANT: Carr, Grant  
APPLICANT: Yamamoto, Robert  
APPLICANT: Forsyth, R.  
APPLICANT: Xu, H.  
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms  
FILE REFERENCE: ELITRA.034A  
CURRENT APPLICATION NUMBER: US/10/282.122A  
CURRENT FILING DATE: 2003-02-20  
PRIOR APPLICATION NUMBER: 60/191,078  
PRIOR FILING DATE: 2000-03-21  
PRIOR APPLICATION NUMBER: 60/206,848  
PRIOR FILING DATE: 2000-05-23  
PRIOR APPLICATION NUMBER: 60/207,727  
PRIOR FILING DATE: 2000-05-26  
PRIOR APPLICATION NUMBER: 60/230,335  
PRIOR FILING DATE: 2000-09-06  
PRIOR APPLICATION NUMBER: 60/230,347  
PRIOR FILING DATE: 2000-09-09  
PRIOR APPLICATION NUMBER: 60/242,578  
PRIOR FILING DATE: 2000-10-23  
PRIOR APPLICATION NUMBER: 60/253,625  
PRIOR FILING DATE: 2000-11-27  
PRIOR APPLICATION NUMBER: 60/257,931  
PRIOR FILING DATE: 2000-12-22

PRIOR APPLICATION NUMBER: 60/267,636  
PRIOR FILING DATE: 2001-02-09  
PRIOR APPLICATION NUMBER: 60/269,308  
PRIOR FILING DATE: 2001-02-16  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 78614  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 43351  
LENGTH: 432  
TYPE: PRF  
ORGANISM: Escherichia coli  
US-10-282-122A-43351

Query Match 96.6%; Score 2182; DB 12; Length 432;  
Best Local Similarity 98.1%; Pred. No. 7.6e-201;  
Matches 424; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 MKAILIPFLSLIPLTPQSAFAQSEPELKESVIVSRHGVRAPTKATQTMQDVTPDAMP 60  
1 MKAILIPFLSLIPLTPQSAFAQSEPELKESVIVSRHGVRAPTKATQTMQDVTPDAMP 60

Db 61 TWPVKLGELTPRGSELIAVIGHYWRQRLVADGLPKCCGPOSGOVAIADVDERTKGTGE 120  
61 TWPVKLGELTPRGSELIAVIGHYWRQRLVADGLPKCCGPOSGOVAIADVDERTKGTGE 120

QY 121 APAAGLAPDCAITVHTQADTSSPDLEFNPLKTGVCQLDNANVTDAILERAGGSIAIDFTGH 180  
121 APAAGLAPDCAITVHTQADTSSPDLEFNPLKTGVCQLDNANVTDAILERAGGSIAIDFTGH 180

Db 121 APAAGLAPDCAITVHTQADTSSPDLEFNPLKTGVCQLDNANVTDAILERAGGSIAIDFTGH 180  
121 APAAGLAPDCAITVHTQADTSSPDLEFNPLKTGVCQLDNANVTDAILERAGGSIAIDFTGH 180

QY 181 YOTAFRELERVLPQSNLCLKREKODESCSLTQALPSELKVSADCVSLTGAVSLASMLT 240  
181 YOTAFRELERVLPQSNLCLKREKODESCSLTQALPSELKVSADCVSLTGAVSLASMLT 240

Db 181 YOTAFRELERVLPQSNLCLKREKODESCSLTQALPSELKVSADCVSLTGAVSLASMLT 240  
181 YOTAFRELERVLPQSNLCLKREKODESCSLTQALPSELKVSADCVSLTGAVSLASMLT 240

QY 241 EIFLLQQAQMPGPGNGRITDSHQWNTLLSLHNAQFLLQRTPEVASRATPLDLIKTA 300  
241 EIFLLQQAQMPGPGNGRITDSHQWNTLLSLHNAQFLLQRTPEVASRATPLDLIKTA 300

Db 241 EIFLLQQAQMPGPGNGRITDSHQWNTLLSLHNAQFLLQRTPEVASRATPLDLIKTA 300  
241 EIFLLQQAQMPGPGNGRITDSHQWNTLLSLHNAQFLLQRTPEVASRATPLDLIKTA 300

QY 301 LTPHPQKQAYGVLPTSVLFIAGHDNTLANLGGALBLNMTLPGQPDNTPPGSELVFERW 360  
301 LTPHPQKQAYGVLPTSVLFIAGHDNTLANLGGALBLNMTLPGQPDNTPPGSELVFERW 360

Db 301 LTPHPQKQAYGVLPTSVLFIAGHDNTLANLGGALBLNMTLPGQPDNTPPGSELVFERW 360  
301 LTPHPQKQAYGVLPTSVLFIAGHDNTLANLGGALBLNMTLPGQPDNTPPGSELVFERW 360

QY 361 RRLSDNSQWIVSVFQTLQCMRDKTPSLNTPGEXKLTLAGCEERNAQMGSLAGFTQ 420  
361 RRLSDNSQWIVSVFQTLQCMRDKTPSLNTPGEXKLTLAGCEERNAQMGSLAGFTQ 420

Db 361 RRLSDNSQWIVSVFQTLQCMRDKTPSLNTPGEXKLTLAGCEERNAQMGSLAGFTQ 420  
361 RRLSDNSQWIVSVFQTLQCMRDKTPSLNTPGEXKLTLAGCEERNAQMGSLAGFTQ 420

QY 421 IVNEARIPACSL 432  
421 IVNEARIPACSL 432

Db 421 IVNEARIPACSL 432  
421 IVNEARIPACSL 432

RESULT 5  
US-10-156-660-4  
Sequence 4, Application US/10156660  
Publication No. US20030103958A1  
GENERAL INFORMATION:  
APPLICANT: Short, Jay M.  
APPLICANT: Kretz, Keith  
APPLICANT: Gray, Kevin A.  
APPLICANT: Barton, Nelson R.  
APPLICANT: Garrett, James B.  
APPLICANT: O'Donoghue, Eileen  
APPLICANT: Mathur, Eric J.  
TITLE OF INVENTION: PHYLAKS, NUCLEIC ACIDS ENCODING THEM  
TITLE OF INVENTION: AND METHODS FOR MAKING AND USING THEM  
FILE REFERENCE: 09010-029007  
CURRENT APPLICATION NUMBER: US/10/156,660  
CURRENT FILING DATE: 2002-10-01  
PRIOR APPLICATION NUMBER: US 09/866,379  
PRIOR FILING DATE: 2001-05-24  
PRIOR APPLICATION NUMBER: US 09/580,515  
PRIOR FILING DATE: 2000-05-25  
PRIOR APPLICATION NUMBER: US 09/318,528  
PRIOR FILING DATE: 1999-05-25



; PRIOR APPLICATION NUMBER: US 09/291,931  
 ; PRIOR FILING DATE: 1999-04-13  
 ; PRIOR APPLICATION NUMBER: US 09/259,214  
 ; PRIOR FILING DATE: 1999-03-01  
 ; PRIOR APPLICATION NUMBER: US 08/910,798  
 ; PRIOR FILING DATE: 1997-08-13  
 ; NUMBER OF SEQ ID NOS: 4  
 ; SOFTWARE: FASTSEQ for Windows Version 4.0  
 ; SEQ ID NO 4  
 ; LENGTH: 432  
 ; TYPE: PRK  
 ; ORGANISM: Escherichia coli  
 ; US-10-156-660-4

Query Match 96.6%; Score 2182; DB 14; Length 432;  
 Best Local Similarity 98.1%; Pred. No. 7.6e-201;  
 Matches 424; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 MKAILIPFLSLIPLPQSAFAQSEPELKESVIVSRHGVRAPTKATQLMQDVTDPAMP 60  
 DB 1 MKAILIPFLSLIPLPQSAFAQSEPELKESVIVSRHGVRAPTKATQLMQDVTDPAMP 60  
 QY 61 TWPVKLGELTPRGSELIAVIGHYQRQLVADGLPKCGCPQSGQVAIIADVDERTKTGE 120  
 DB 61 TWPVKLGELTPRGSELIAVIGHYQRQLVADGLPKCGCPQSGQVAIIADVDERTKTGE 120  
 QY 121 AFAAGLAPDCAITVHTQADTSSPDLPFNPLKTVGCQLDNNAVTDAILERAGGSIAADFTGH 180  
 DB 121 AFAAGLAPDCAITVHTQADTSSPDLPFNPLKTVGCQLDNNAVTDAILERAGGSIAADFTGH 180  
 QY 121 AFAAGLAPDCAITVHTQADTSSPDLPFNPLKTVGCQLDNNAVTDAILERAGGSIAADFTGH 180  
 DB 121 AFAAGLAPDCAITVHTQADTSSPDLPFNPLKTVGCQLDNNAVTDAILERAGGSIAADFTGH 180  
 QY 181 YOTAFRELERVLPQSNCLKREKODESCSLTQALPELKVSDCVSLTGVASLASMLT 240  
 DB 181 YOTAFRELERVLPQSNCLKREKODESCSLTQALPELKVSDCVSLTGVASLASMLT 240  
 QY 181 YOTAFRELERVLPQSNCLKREKODESCSLTQALPELKVSDCVSLTGVASLASMLT 240  
 DB 181 YOTAFRELERVLPQSNCLKREKODESCSLTQALPELKVSDCVSLTGVASLASMLT 240  
 QY 241 EIFLLQAOQMPBPQGRITDSHQWNTLLSLHNAQFDLQTPVARSRAIPLLDLIKTA 300  
 DB 241 EIFLLQAOQMPBPQGRITDSHQWNTLLSLHNAQFDLQTPVARSRAIPLLDLIKTA 300  
 QY 301 LTPHPQKQAYGVTLPTSVLFIAGHDNLNANLGALELNTLTPQDPNTPPGSELVEERW 360  
 DB 301 LTPHPQKQAYGVTLPTSVLFIAGHDNLNANLGALELNTLTPQDPNTPPGSELVEERW 360  
 QY 301 LTPHPQKQAYGVTLPTSVLFIAGHDNLNANLGALELNTLTPQDPNTPPGSELVEERW 360  
 DB 301 LTPHPQKQAYGVTLPTSVLFIAGHDNLNANLGALELNTLTPQDPNTPPGSELVEERW 360  
 QY 361 RLSDNSQMIQVSLVFQTLQQRDKTLPISLNTPPGEVXLTLAGCEBRNAQMCISLAGFTQ 420  
 DB 361 RLSDNSQMIQVSLVFQTLQQRDKTLPISLNTPPGEVXLTLAGCEBRNAQMCISLAGFTQ 420  
 QY 421 IYNEARIPACSL 432  
 DB 421 IYNEARIPACSL 432

RESULT 6  
 US-09-777-566A-2  
 ; Sequence 2, Application US/09777566A  
 ; Patent No. US20010055788A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: DIVERSA CORPORATION  
 ; APPLICANT: SHORT, Jay  
 ; APPLICANT: KREITZ, Keith  
 ; TITLE OF INVENTION: RECOMBINANT BACTERIAL PHRYASES AND USES THEREOF  
 ; FILE REFERENCE: DIVER1370-6  
 ; CURRENT APPLICATION NUMBER: US/09/777,566A  
 ; PRIOR FILING DATE: 2001-06-11  
 ; PRIOR APPLICATION NUMBER: US 09/318,528  
 ; PRIOR FILING DATE: 1999-05-25  
 ; PRIOR APPLICATION NUMBER: US 09/291,931  
 ; PRIOR FILING DATE: 1999-04-13  
 ; PRIOR APPLICATION NUMBER: US 09/259,214  
 ; PRIOR FILING DATE: 1999-03-01  
 ; PRIOR APPLICATION NUMBER: US 08/910,798  
 ; PRIOR FILING DATE: 1997-08-13  
 ; NUMBER OF SEQ ID NOS: 4  
 ; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 2  
 ; LENGTH: 440  
 ; TYPE: PRK  
 ; ORGANISM: Escherichia coli  
 ; FEATURE:  
 ; NAME/KEY: misc.feature  
 ; LOCATION: (1)..(1323)  
 ; OTHER INFORMATION: n is any nucleotide  
 ; US-09-777-566A-2

Query Match 96.1%; Score 2171; DB 9; Length 440;  
 Best Local Similarity 97.7%; Pred. No. 8.9e-200;  
 Matches 422; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 1 MKAILIPFLSLIPLPQSAFAQSEPELKESVIVSRHGVRAPTKATQLMQDVTDPAMP 60  
 DB 1 MKAILIPFLSLIPLPQSAFAQSEPELKESVIVSRHGVRAPTKATQLMQDVTDPAMP 60  
 QY 61 TWPVKLGELTPRGSELIAVIGHYQRQLVADGLPKCGCPQSGQVAIIADVDERTKTGE 120  
 DB 61 TWPVKLGELTPRGSELIAVIGHYQRQLVADGLPKCGCPQSGQVAIIADVDERTKTGE 120  
 QY 121 AFAAGLAPDCAITVHTQADTSSPDLPFNPLKTVGCQLDNNAVTDAILERAGGSIAADFTGH 180  
 DB 121 AFAAGLAPDCAITVHTQADTSSPDLPFNPLKTVGCQLDNNAVTDAILERAGGSIAADFTGH 180  
 QY 121 AFAAGLAPDCAITVHTQADTSSPDLPFNPLKTVGCQLDNNAVTDAILERAGGSIAADFTGH 180  
 DB 121 AFAAGLAPDCAITVHTQADTSSPDLPFNPLKTVGCQLDNNAVTDAILERAGGSIAADFTGH 180  
 QY 181 YOTAFRELERVLPQSNCLKREKODESCSLTQALPELKVSDCVSLTGVASLASMLT 240  
 DB 181 YOTAFRELERVLPQSNCLKREKODESCSLTQALPELKVSDCVSLTGVASLASMLT 240  
 QY 181 YOTAFRELERVLPQSNCLKREKODESCSLTQALPELKVSDCVSLTGVASLASMLT 240  
 DB 181 YOTAFRELERVLPQSNCLKREKODESCSLTQALPELKVSDCVSLTGVASLASMLT 240  
 QY 241 EIFLLQAOQMPBPQGRITDSHQWNTLLSLHNAQFDLQTPVARSRAIPLLDLIKTA 300  
 DB 241 EIFLLQAOQMPBPQGRITDSHQWNTLLSLHNAQFDLQTPVARSRAIPLLDLIKTA 300  
 QY 241 EIFLLQAOQMPBPQGRITDSHQWNTLLSLHNAQFDLQTPVARSRAIPLLDLIKTA 300  
 DB 241 EIFLLQAOQMPBPQGRITDSHQWNTLLSLHNAQFDLQTPVARSRAIPLLDLIKTA 300  
 QY 301 LTPHPQKQAYGVTLPTSVLFIAGHDNLNANLGALELNTLTPQDPNTPPGSELVEERW 360  
 DB 301 LTPHPQKQAYGVTLPTSVLFIAGHDNLNANLGALELNTLTPQDPNTPPGSELVEERW 360  
 QY 301 LTPHPQKQAYGVTLPTSVLFIAGHDNLNANLGALELNTLTPQDPNTPPGSELVEERW 360  
 DB 301 LTPHPQKQAYGVTLPTSVLFIAGHDNLNANLGALELNTLTPQDPNTPPGSELVEERW 360  
 QY 361 RLSDNSQMIQVSLVFQTLQQRDKTLPISLNTPPGEVXLTLAGCEBRNAQMCISLAGFTQ 420  
 DB 361 RLSDNSQMIQVSLVFQTLQQRDKTLPISLNTPPGEVXLTLAGCEBRNAQMCISLAGFTQ 420  
 QY 421 IYNEARIPACSL 432  
 DB 421 IYNEARIPACSL 432

RESULT 7  
 US-09-866-379-2  
 ; Sequence 2, Application US/09866379  
 ; Patent No. US20020136754A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: DIVERSA CORPORATION  
 ; APPLICANT: SHORT, Jay  
 ; APPLICANT: KREITZ, Keith  
 ; APPLICANT: GRAY, Kevin  
 ; APPLICANT: BARTON, Nelson  
 ; APPLICANT: GARRETT, James  
 ; APPLICANT: O'DONOGHUE, Eileen  
 ; TITLE OF INVENTION: RECOMBINANT BACTERIAL PHRYASES AND USES THEREOF  
 ; FILE REFERENCE: DIVER1370-7  
 ; CURRENT APPLICATION NUMBER: US/09/866,379  
 ; PRIOR FILING DATE: 2001-05-24  
 ; PRIOR APPLICATION NUMBER: US 09/580,515  
 ; PRIOR FILING DATE: 2000-05-25  
 ; PRIOR APPLICATION NUMBER: US 09/318,528  
 ; PRIOR FILING DATE: 1999-05-25  
 ; PRIOR APPLICATION NUMBER: US 09/291,931  
 ; PRIOR FILING DATE: 1999-04-13  
 ; PRIOR APPLICATION NUMBER: US 09/259,214  
 ; PRIOR FILING DATE: 1999-03-01  
 ; PRIOR APPLICATION NUMBER: US 08/910,798  
 ; PRIOR FILING DATE: 1997-08-13

NUMBER OF SEQ ID NOS: 10  
SOFTWARE: Patent version 3.1  
SEQ ID NO 2  
LENGTH: 440  
TYPE: PRT  
ORGANISM: Escherichia coli  
US-09-866-379-2

Query Match 96.1%; Score 2171; DB 9; Length 440;  
Best Local Similarity 97.7%; Pred. No. 8.9e-200;

Matches 422; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

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QY 1 MKAIIIPFSLILPLTPQSAFAQSEPELKESVIVSRHGVRAPTKATQLMQDVTDPDAMP 60
DB 1 MKAIIIPFSLILPLTPQSAFAQSEPELKESVIVSRHGVRAPTKATQLMQDVTDPDAMP 60
QY 61 TWPVKLGELTPRGGEIAYIGHYMRQRLVADGLLPKCGCPQSGQVAILADVDETRKTGE 120
DB 61 TWPVKLGELTPRGGEIAYIGHYMRQRLVADGLLPKCGCPQSGQVAILADVDETRKTGE 120
QY 121 APAAGLAPDCAITVHTQADTSSPDLFENPKTGVCQLDNANVTDAILERAGSIADEFTH 180
DB 121 APAAGLAPDCAITVHTQADTSSPDLFENPKTGVCQLDNANVTDAILERAGSIADEFTH 180
QY 121 APAAGLAPDCAITVHTQADTSSPDLFENPKTGVCQLDNANVTDAILERAGSIADEFTH 180
DB 121 APAAGLAPDCAITVHTQADTSSPDLFENPKTGVCQLDNANVTDAILERAGSIADEFTH 180
QY 181 YOTAFRELERVLPQSNCLKREKODESCSLTOALPSELKVSADVSLTGAVSLASMLT 240
DB 181 YOTAFRELERVLPQSNCLKREKODESCSLTOALPSELKVSADVSLTGAVSLASMLT 240
QY 181 YOTAFRELERVLPQSNCLKREKODESCSLTOALPSELKVSADVSLTGAVSLASMLT 240
DB 181 YOTAFRELERVLPQSNCLKREKODESCSLTOALPSELKVSADVSLTGAVSLASMLT 240
QY 241 EIFLLQQAQMPGPGGRITDSHQWNTLLSLHNAQFYLLQRTPEVARSATPLDLIKTA 300
DB 241 EIFLLQQAQMPGPGGRITDSHQWNTLLSLHNAQFYLLQRTPEVARSATPLDLIKTA 300
QY 241 EIFLLQQAQMPGPGGRITDSHQWNTLLSLHNAQFYLLQRTPEVARSATPLDLIKTA 300
DB 241 EIFLLQQAQMPGPGGRITDSHQWNTLLSLHNAQFYLLQRTPEVARSATPLDLIKTA 300
QY 301 LTPHPQKQAYGVTLPTSVLFIAGHDTNLANLGGALBNMTLPGQPDNTPPGGELVFERW 360
DB 301 LTPHPQKQAYGVTLPTSVLFIAGHDTNLANLGGALBNMTLPGQPDNTPPGGELVFERW 360
QY 361 RLSDNSQWIOVSLVFQTLQQRDKTPLSLNTPPGEVKLTLAGCERNNAQMGCSLAGFTQ 420
DB 361 RLSDNSQWIOVSLVFQTLQQRDKTPLSLNTPPGEVKLTLAGCERNNAQMGCSLAGFTQ 420
QY 421 IYNEARIPACSL 432
DB 421 IYNEARIPACSL 432
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RESULT 8  
US-10-034-985-2

Sequence 2, Application US/10034985  
Publication No. US20030049815A1  
GENERAL INFORMATION:  
APPLICANT: Kretz, Keith  
TITLE OF INVENTION: NOVEL PHYTASE  
FILE REFERENCE: 09010/029003  
CURRENT APPLICATION NUMBER: US/10/034,985  
PRIOR FILING DATE: 2001-12-21  
PRIOR APPLICATION NUMBER: US/09/580,515  
PRIOR FILING DATE: 1999-05-25  
PRIOR APPLICATION NUMBER: 09/291,931  
PRIOR FILING DATE: 1999-04-13  
PRIOR APPLICATION NUMBER: 08/910,798  
PRIOR FILING DATE: 1997-08-13  
PRIOR APPLICATION NUMBER: 09/259,214  
PRIOR FILING DATE: 1999-03-01  
NUMBER OF SEQ ID NOS: 4  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 2  
LENGTH: 440  
TYPE: PRT  
ORGANISM: Escherichia coli  
US-10-034-985-2

Query Match 96.1%; Score 2171; DB 14; Length 440;  
Best Local Similarity 97.7%; Pred. No. 8.9e-200;

Matches 422; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

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QY 1 MKAIIIPFSLILPLTPQSAFAQSEPELKESVIVSRHGVRAPTKATQLMQDVTDPDAMP 60
DB 1 MKAIIIPFSLILPLTPQSAFAQSEPELKESVIVSRHGVRAPTKATQLMQDVTDPDAMP 60
QY 61 TWPVKLGELTPRGGEIAYIGHYMRQRLVADGLLPKCGCPQSGQVAILADVDETRKTGE 120
DB 61 TWPVKLGELTPRGGEIAYIGHYMRQRLVADGLLPKCGCPQSGQVAILADVDETRKTGE 120
QY 121 APAAGLAPDCAITVHTQADTSSPDLFENPKTGVCQLDNANVTDAILERAGSIADEFTH 180
DB 121 APAAGLAPDCAITVHTQADTSSPDLFENPKTGVCQLDNANVTDAILERAGSIADEFTH 180
QY 121 APAAGLAPDCAITVHTQADTSSPDLFENPKTGVCQLDNANVTDAILERAGSIADEFTH 180
DB 121 APAAGLAPDCAITVHTQADTSSPDLFENPKTGVCQLDNANVTDAILERAGSIADEFTH 180
QY 181 YOTAFRELERVLPQSNCLKREKODESCSLTOALPSELKVSADVSLTGAVSLASMLT 240
DB 181 YOTAFRELERVLPQSNCLKREKODESCSLTOALPSELKVSADVSLTGAVSLASMLT 240
QY 181 YOTAFRELERVLPQSNCLKREKODESCSLTOALPSELKVSADVSLTGAVSLASMLT 240
DB 181 YOTAFRELERVLPQSNCLKREKODESCSLTOALPSELKVSADVSLTGAVSLASMLT 240
QY 241 EIFLLQQAQMPGPGGRITDSHQWNTLLSLHNAQFYLLQRTPEVARSATPLDLIKTA 300
DB 241 EIFLLQQAQMPGPGGRITDSHQWNTLLSLHNAQFYLLQRTPEVARSATPLDLIKTA 300
QY 241 EIFLLQQAQMPGPGGRITDSHQWNTLLSLHNAQFYLLQRTPEVARSATPLDLIKTA 300
DB 241 EIFLLQQAQMPGPGGRITDSHQWNTLLSLHNAQFYLLQRTPEVARSATPLDLIKTA 300
QY 301 LTPHPQKQAYGVTLPTSVLFIAGHDTNLANLGGALBNMTLPGQPDNTPPGGELVFERW 360
DB 301 LTPHPQKQAYGVTLPTSVLFIAGHDTNLANLGGALBNMTLPGQPDNTPPGGELVFERW 360
QY 361 RLSDNSQWIOVSLVFQTLQQRDKTPLSLNTPPGEVKLTLAGCERNNAQMGCSLAGFTQ 420
DB 361 RLSDNSQWIOVSLVFQTLQQRDKTPLSLNTPPGEVKLTLAGCERNNAQMGCSLAGFTQ 420
QY 421 IYNEARIPACSL 432
DB 421 IYNEARIPACSL 432
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RESULT 9

US-10-430-356-2  
Sequence 2, Application US/10430356  
Publication No. US2003023041A1  
GENERAL INFORMATION:  
APPLICANT: Kretz, Keith  
TITLE OF INVENTION: NOVEL PHYTASE  
FILE REFERENCE: 09010/029003  
CURRENT APPLICATION NUMBER: US/10/430,356  
PRIOR FILING DATE: 2003-05-05  
PRIOR APPLICATION NUMBER: 09/318,528  
PRIOR FILING DATE: 1999-05-25  
PRIOR APPLICATION NUMBER: 09/291,931  
PRIOR FILING DATE: 1999-04-13  
PRIOR APPLICATION NUMBER: 08/910,798  
PRIOR FILING DATE: 1997-08-13  
PRIOR APPLICATION NUMBER: 09/259,214  
PRIOR FILING DATE: 1999-03-01  
NUMBER OF SEQ ID NOS: 4  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 2  
LENGTH: 440  
TYPE: PRT  
ORGANISM: Escherichia coli  
US-10-430-356-2

Query Match 96.1%; Score 2171; DB 15; Length 440;  
Best Local Similarity 97.7%; Pred. No. 8.9e-200;

Matches 422; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

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QY 1 MKAIIIPFSLILPLTPQSAFAQSEPELKESVIVSRHGVRAPTKATQLMQDVTDPDAMP 60
DB 1 MKAIIIPFSLILPLTPQSAFAQSEPELKESVIVSRHGVRAPTKATQLMQDVTDPDAMP 60
QY 61 TWPVKLGELTPRGGEIAYIGHYMRQRLVADGLLPKCGCPQSGQVAILADVDETRKTGE 120
DB 61 TWPVKLGELTPRGGEIAYIGHYMRQRLVADGLLPKCGCPQSGQVAILADVDETRKTGE 120
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Db 61 TWPVKGLWLTGRGELLAYLGHYORRLVADGLLAKKGCPOSGQVAILADVDERTRKTC 120

Qy 121 AFAAGLADCAITVHTQADTSSPDLFNPILKTCQGLDNNVMTALLERAGSIAADTGH 180

Db 121 AFAAGLADCAITVHTQADTSSPDLFNPILKTCQGLDNNVMTALLERAGSIAADTGH 180

Qy 181 YQTAFFRELEVLNFPQSNLCKREKODSCSLTQALPSELKVSADCVSLTGAVSLASMLT 240

Db 181 RQTAFFRELEVLNFPQSNLCKREKODSCSLTQALPSELKVSADCVSLTGAVSLASMLT 240

Qy 241 EIFFLQOAGQMPBPWGKRTTDSHQMNTLLSLHNAQFLLQSTPEVARSRAPIPLDLIKTA 300

Db 241 EIFFLQOAGQMPBPWGKRTTDSHQMNTLLSLHNAQFLLQSTPEVARSRAPIPLDLIKTA 300

Qy 301 LTPHPPOKQAVGVTLPSTVLFAGHDTNLANLGALEINMTLPQGPDPNTPPGSELVEERW 360

Db 301 LTPHPPOKQAVGVTLPSTVLFAGHDTNLANLGALEINMTLPQGPDPNTPPGSELVEERW 360

Qy 361 RLSDNSQMTQVSLVFQTLQONRDKTPISLNTPPGEVKLTLAGCEERNAQMGCSLAGFTQ 420

Db 361 RLSDNSQMTQVSLVFQTLQONRDKTPISLNTPPGEVKLTLAGCEERNAQMGCSLAGFTQ 420

Qy 421 IYNEARIPACSL 432

Db 421 IYNEARIPACSL 432

## RESULT 10

US-10-334-672-1

Sequence 1, Application US/10334672

Publication No. US20030157646A1

GENERAL INFORMATION:

APPLICANT: Lananan, Mike

APPLICANT: Koeft, Edward

APPLICANT: Kretz, Keith

TITLE OF INVENTION: Microbially-Expressed Thermotolerant Phytase For Animal Feed

FILE REFERENCE: SYNG-P01-001

CURRENT APPLICATION NUMBER: US/10/334,672

CURRENT FILING DATE: 2002-12-30

PRIOR APPLICATION NUMBER: 60/344,523

PRIOR FILING DATE: 2001-12-28

NUMBER OF SEQ ID NOS: 4

SOFTWARE: Patentin version 3.1

SEQ ID NO 1

LENGTH: 412

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: No. US20030157646A19X Phytase

US-10-334-672-1

Query Match 95.5%; Score 2157; DB 14; Length 412;

Best Local Similarity 100.0%; Pred. No. 1.8e-198;

Matches 411; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 22 AOSEBELKLESVIVSRHGVRAPTKATQIMQDVTDPAMTFWVKLGELTPRGELIAYLG 81

Db 2 AOSEBELKLESVIVSRHGVRAPTKATQIMQDVTDPAMTFWVKLGELTPRGELIAYLG 81

Qy 82 HWRRORLIVADGLLPKCGCPQSGQVAILADVDERTRKTCGAPAGLAPDCAITVHTQADTS 141

Db 62 HWRRORLIVADGLLPKCGCPQSGQVAILADVDERTRKTCGAPAGLAPDCAITVHTQADTS 121

Qy 142 SPDPLENPILKTCQGLDNNVMTALLERAGSIAADTGHYQTAFFRELEVLNFPQSNLCL 201

Db 122 SPDPLENPILKTCQGLDNNVMTALLERAGSIAADTGHYQTAFFRELEVLNFPQSNLCL 181

Qy 202 KREKODSCSLTQALPSELKVSADCVSLTGAVSLASMLTEIFFLQOAGQMPBPWGKRTT 261

Db 182 KREKODSCSLTQALPSELKVSADCVSLTGAVSLASMLTEIFFLQOAGQMPBPWGKRTT 241

Qy 262 SHQWNTLLSLHNAQFLLQSTPEVARSRAPIPLDLIKTALTPHPPOKQAVGVTLPSTVLF 321

Db 262 SHQWNTLLSLHNAQFLLQSTPEVARSRAPIPLDLIKTALTPHPPOKQAVGVTLPSTVLF 321

Db 242 SHQWNTLLSLHNAQFLLQSTPEVARSRAPIPLDLIKTALTPHPPOKQAVGVTLPSTVLF 301

Qy 322 IAGHDTNLANLGALEINMTLPQGPDPNTPPGSELVEERMRRLSDNSQMTQVSLVFQTLQ 381

Db 302 IAGHDTNLANLGALEINMTLPQGPDPNTPPGSELVEERMRRLSDNSQMTQVSLVFQTLQ 361

Qy 382 MDKTPISLNTPPGEVKLTLAGCEERNAQMGCSLAGFTQIYNEARIPACSL 432

Db 362 MDKTPISLNTPPGEVKLTLAGCEERNAQMGCSLAGFTQIYNEARIPACSL 412

## RESULT 11

US-10-334-671-1

Sequence 1, Application US/10334671

Publication No. US20030170293A1

GENERAL INFORMATION:

APPLICANT: Lananan, Mike

APPLICANT: Koeft, Edward

APPLICANT: Kretz, Keith

TITLE OF INVENTION: Microbially-Expressed Thermotolerant Phytase For Animal Feed

FILE REFERENCE: 70098

CURRENT APPLICATION NUMBER: US/10/334,671

CURRENT FILING DATE: 2002-12-30

PRIOR APPLICATION NUMBER: 60/344,523

PRIOR FILING DATE: 2001-12-28

NUMBER OF SEQ ID NOS: 4

SOFTWARE: Patentin version 3.1

SEQ ID NO 1

LENGTH: 412

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: No. US20030170293A19X Phytase

US-10-334-671-1

Query Match 95.5%; Score 2157; DB 14; Length 412;

Best Local Similarity 100.0%; Pred. No. 1.8e-198;

Matches 411; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 22 AOSEBELKLESVIVSRHGVRAPTKATQIMQDVTDPAMTFWVKLGELTPRGELIAYLG 81

Db 2 AOSEBELKLESVIVSRHGVRAPTKATQIMQDVTDPAMTFWVKLGELTPRGELIAYLG 61

Qy 82 HWRRORLIVADGLLPKCGCPQSGQVAILADVDERTRKTCGAPAGLAPDCAITVHTQADTS 141

Db 62 HWRRORLIVADGLLPKCGCPQSGQVAILADVDERTRKTCGAPAGLAPDCAITVHTQADTS 121

Qy 142 SPDPLENPILKTCQGLDNNVMTALLERAGSIAADTGHYQTAFFRELEVLNFPQSNLCL 201

Db 122 SPDPLENPILKTCQGLDNNVMTALLERAGSIAADTGHYQTAFFRELEVLNFPQSNLCL 181

Qy 202 KREKODSCSLTQALPSELKVSADCVSLTGAVSLASMLTEIFFLQOAGQMPBPWGKRTT 261

Db 182 KREKODSCSLTQALPSELKVSADCVSLTGAVSLASMLTEIFFLQOAGQMPBPWGKRTT 241

Qy 262 SHQWNTLLSLHNAQFLLQSTPEVARSRAPIPLDLIKTALTPHPPOKQAVGVTLPSTVLF 321

Db 242 SHQWNTLLSLHNAQFLLQSTPEVARSRAPIPLDLIKTALTPHPPOKQAVGVTLPSTVLF 301

Qy 322 IAGHDTNLANLGALEINMTLPQGPDPNTPPGSELVEERMRRLSDNSQMTQVSLVFQTLQ 381

Db 302 IAGHDTNLANLGALEINMTLPQGPDPNTPPGSELVEERMRRLSDNSQMTQVSLVFQTLQ 361

Qy 382 MDKTPISLNTPPGEVKLTLAGCEERNAQMGCSLAGFTQIYNEARIPACSL 432

Db 362 MDKTPISLNTPPGEVKLTLAGCEERNAQMGCSLAGFTQIYNEARIPACSL 412

## RESULT 12

US-10-021-723A-13

Sequence 13, Application US/10021723A

Publication No. US20030101476A1

GENERAL INFORMATION:

```

/ APPLICANT: Short, Jay
/ APPLICANT: Mathur, Eric
/ APPLICANT: Richardson, Toby
/ APPLICANT: Robertson, Dan
/ APPLICANT: Barton, Nelson
/ TITLE OF INVENTION: Recombinant Phytases and Uses Thereof
/ FILE REFERENCE: 112766.140 (DIV-016CIP)
/ CURRENT APPLICATION NUMBER: US/10/021.723A
/ PRIOR FILING DATE: 2002-10-23
/ PRIOR APPLICATION NUMBER: US 60/255,090
/ PRIOR FILING DATE: 2000-12-12
/ NUMBER OF SEQ ID NOS: 74
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 13
/ LENGTH: 410
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: amino acid sequence of a phytase enzyme with
/ OTHER INFORMATION: predicted glycosylation sites
US-10-021-723A-13

```

```

Query Match          95.3%; Score 2153; DB 14; Length 410;
Best Local Similarity 100.0%; Pred. No. 4.3e-198;
Matches 410; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 23 QSEBELKESVIVSRHGVRAPTKATQIMQDVTDPAMPVVKLGELTPRGELIAYIGH 82
DB 1 QSEBELKESVIVSRHGVRAPTKATQIMQDVTDPAMPVVKLGELTPRGELIAYIGH 60
QY 83 YMRRLVADGGLPKCGCPQSGVAIIADVDERTKRTGEAPAGIAPDCAITVHTQADTSS 142
DB 61 YMRRLVADGGLPKCGCPQSGVAIIADVDERTKRTGEAPAGIAPDCAITVHTQADTSS 120
QY 143 PDPLFNPILKTGVCQLDNANVTDAILERAGSIADFTGHYQTAFFELERVLNFPQSNCLK 202
DB 121 PDPLFNPILKTGVCQLDNANVTDAILERAGSIADFTGHYQTAFFELERVLNFPQSNCLK 180
QY 203 REKODESGSLTQALPSELKVSADCVSLTGAVSLASMLTEIFLLQQAQMPERGWRITDS 262
DB 181 REKODESGSLTQALPSELKVSADCVSLTGAVSLASMLTEIFLLQQAQMPERGWRITDS 240
QY 263 HQWNTLLSIHNAQFDLQRTPEVARSRATPLLDLIKALTPHPQKQAYGTLPTSVLFI 322
DB 241 HQWNTLLSIHNAQFDLQRTPEVARSRATPLLDLIKALTPHPQKQAYGTLPTSVLFI 300
QY 323 AGHDTNLANLGGALFLNMTLPGQPDNTPPGGELVFERRRRLSDNSQWTVSVFQTLQOM 382
DB 301 AGHDTNLANLGGALFLNMTLPGQPDNTPPGGELVFERRRRLSDNSQWTVSVFQTLQOM 360
QY 383 RDKTPLSLNTPPGGEVLTLAGCEERNAQMCSLAGFTQIVNEARIIPACSL 432
DB 361 RDKTPLSLNTPPGGEVLTLAGCEERNAQMCSLAGFTQIVNEARIIPACSL 410

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```

RESULT 13
US-10-021-723A-15
/ Sequence 15, Application US/10021723A
/ Publication No. US20030101476A1
/ GENERAL INFORMATION:
/ APPLICANT: Short, Jay
/ APPLICANT: Mathur, Eric
/ APPLICANT: Richardson, Toby
/ APPLICANT: Robertson, Dan
/ APPLICANT: Barton, Nelson
/ TITLE OF INVENTION: Recombinant Phytases and Uses Thereof
/ FILE REFERENCE: 112766.140 (DIV-016CIP)
/ CURRENT APPLICATION NUMBER: US/10/021.723A
/ PRIOR FILING DATE: 2002-10-23
/ PRIOR APPLICATION NUMBER: US 60/255,090
/ PRIOR FILING DATE: 2000-12-12
/ NUMBER OF SEQ ID NOS: 74
/ SOFTWARE: FastSeq for Windows Version 4.0

```

```

/ SEQ ID NO 15
/ LENGTH: 410
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: amino acid sequence of a phytase enzyme with
/ OTHER INFORMATION: predicted glycosylation sites
US-10-021-723A-15

```

```

Query Match          95.3%; Score 2153; DB 14; Length 410;
Best Local Similarity 100.0%; Pred. No. 4.3e-198;
Matches 410; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 23 QSEBELKESVIVSRHGVRAPTKATQIMQDVTDPAMPVVKLGELTPRGELIAYIGH 82
DB 1 QSEBELKESVIVSRHGVRAPTKATQIMQDVTDPAMPVVKLGELTPRGELIAYIGH 60
QY 83 YMRRLVADGGLPKCGCPQSGVAIIADVDERTKRTGEAPAGIAPDCAITVHTQADTSS 142
DB 61 YMRRLVADGGLPKCGCPQSGVAIIADVDERTKRTGEAPAGIAPDCAITVHTQADTSS 120
QY 143 PDPLFNPILKTGVCQLDNANVTDAILERAGSIADFTGHYQTAFFELERVLNFPQSNCLK 202
DB 121 PDPLFNPILKTGVCQLDNANVTDAILERAGSIADFTGHYQTAFFELERVLNFPQSNCLK 180
QY 203 REKODESGSLTQALPSELKVSADCVSLTGAVSLASMLTEIFLLQQAQMPERGWRITDS 262
DB 181 REKODESGSLTQALPSELKVSADCVSLTGAVSLASMLTEIFLLQQAQMPERGWRITDS 240
QY 263 HQWNTLLSIHNAQFDLQRTPEVARSRATPLLDLIKALTPHPQKQAYGTLPTSVLFI 322
DB 241 HQWNTLLSIHNAQFDLQRTPEVARSRATPLLDLIKALTPHPQKQAYGTLPTSVLFI 300
QY 323 AGHDTNLANLGGALFLNMTLPGQPDNTPPGGELVFERRRRLSDNSQWTVSVFQTLQOM 382
DB 301 AGHDTNLANLGGALFLNMTLPGQPDNTPPGGELVFERRRRLSDNSQWTVSVFQTLQOM 360
QY 383 RDKTPLSLNTPPGGEVLTLAGCEERNAQMCSLAGFTQIVNEARIIPACSL 432
DB 361 RDKTPLSLNTPPGGEVLTLAGCEERNAQMCSLAGFTQIVNEARIIPACSL 410

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RESULT 14
US-10-284-962-3
/ Sequence 3, Application US/10284962
/ Publication No. US20030206913A1
/ GENERAL INFORMATION:
/ APPLICANT: Webel, Douglas M.
/ APPLICANT: Orr, Donald E.
/ APPLICANT: Rich, Frank E.
/ TITLE OF INVENTION: PHYTASE-CONTAINING ANIMAL FOOD AND METHOD
/ FILE REFERENCE: 834460-71725
/ CURRENT APPLICATION NUMBER: US/10/284,962
/ PRIOR FILING DATE: 2002-10-31
/ PRIOR APPLICATION NUMBER: US 60/335,303
/ PRIOR FILING DATE: 2001-10-31
/ NUMBER OF SEQ ID NOS: 14
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 3
/ LENGTH: 432
/ TYPE: PRT
/ ORGANISM: Escherichia coli
US-10-284-962-3

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```

Query Match          95.1%; Score 2147; DB 15; Length 432;
Best Local Similarity 96.8%; Pred. No. 1.8e-197;
Matches 418; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

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```

QY 1 MKAILIPFSLILPLTPQSAFAQSEBELKESVIVSRHGVRAPTKATQIMQDVTDPAMP 60
DB 1 MKAILIPFSLILPLTPQSAFAQSEBELKESVIVSRHGVRAPTKATQIMQDVTDPAMP 60
QY 61 TWPVKLGELTPRGELIAYIGHYMRRLVADGGLPKCGCPQSGVAIIADVDERTKRTGE 120

```

```
Db 61 TWPKLGMWLPBGGELIAYIGHYORLIVADGLLAKGCCPQGOVALIADVDRRTKTE 120
Qy 121 APAAGLAPDCAITVHTQADTSSPDLFNPPLKTVGCQLDNANVTDAIIEBAGSSIAFTGH 180
Db 121 APAAGLAPDCAITVHTQADTSSPDLFNPPLKTVGCQLDNANVTDAIISBAGSSIAFTGH 180
Qy 181 YQTAERLEEVLANPQSNCLKREKODSCSLTQALSELKVSADCVSLGAVSLASMLT 240
Db 181 RQTAERLEEVLANPQSNCLKREKODSCSLTQALSELKVSADCVSLGAVSLASMLT 240
Qy 241 EIFLLQQAQGWPEBGMGRTSDSHQWNTLLSLHNAQFDLLQRTPEVARSRAATPLIDLITMA 300
Db 241 EIFLLQQAQGWPEBGMGRTSDSHQWNTLLSLHNAQFDLLQRTPEVARSRAATPLIDLITMA 300
Qy 301 LTPHPQQAQAVTLPTSVLFIAGHDNTLANLGALIELNMTLPQOPDNTPPGGELVEERW 360
Db 301 LTPHPQQAQAVTLPTSVLFIAGHDNTLANLGALIELNMTLPQOPDNTPPGGELVEERW 360
Qy 361 RRLSDNSQMIQVSLVFQTLQQRDKTPLSLNTPGGEVCLTLAGEBENNAQMGCSLAGFTQ 420
Db 361 RRLSDNSQMIQVSLVFQTLQQRDKTPLSLNTPGGEVCLTLAGEBENNAQMGCSLAGFTQ 420
Qy 421 IYNEARIPACSL 432
Db 421 IYNEARIPACSL 432
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## RESULT 15

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US-10-284-962-14
; Sequence 14, Application US/10284962
; Publication No. US20030206913A1
; GENERAL INFORMATION:
; APPLICANT: Webel, Douglas M.
; APPLICANT: Orr, Donald E.
; APPLICANT: Ruch, Frank E.
; TITLE OF INVENTION: PHYTASE-CONTAINING ANIMAL FOOD AND METHOD
; FILE REFERENCE: 834460-71725
; CURRENT APPLICATION NUMBER: US/10/284,962
; PRIOR FILING DATE: 2002-10-31
; PRIOR APPLICATION NUMBER: US 60/335,303
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patent version 3.1
; SEQ ID NO 14
; LENGTH: 432
; TYPE: PRT
; ORGANISM: Escherichia coli
US-10-284-962-14
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Query Match 95.1%; Score 2147; DB 15; Length 432;
Best Local Similarity 96.8%; Pred. No. 1.8e-197;
Matches 418; Conservative 0; Mismatches 14; Indels 0; Gaps 0;
Qy 1 MKAILIPFLSLIPLTPQSAFAQSEBELKLSVIVSRHGVRAPTKATQLMODVTPDAMP 60
Db 1 MKAILIPFLSLIPLTPQSAFAQSEBELKLSVIVSRHGVRAPTKATQLMODVTPDAMP 60
Qy 61 TWPVKLGELTPRGELIAYIGHYORLIVADGLLAKGCCPQGOVALIADVDRRTKTE 120
Db 61 TWPVKLGELTPRGELIAYIGHYORLIVADGLLAKGCCPQGOVALIADVDRRTKTE 120
Qy 121 APAAGLAPDCAITVHTQADTSSPDLFNPPLKTVGCQLDNANVTDAIIEBAGSSIAFTGH 180
Db 121 APAAGLAPDCAITVHTQADTSSPDLFNPPLKTVGCQLDNANVTDAIISBAGSSIAFTGH 180
Qy 181 YQTAERLEEVLANPQSNCLKREKODSCSLTQALSELKVSADCVSLGAVSLASMLT 240
Db 181 RQTAERLEEVLANPQSNCLKREKODSCSLTQALSELKVSADCVSLGAVSLASMLT 240
Qy 241 EIFLLQQAQGWPEBGMGRTSDSHQWNTLLSLHNAQFDLLQRTPEVARSRAATPLIDLITMA 300
Db 241 EIFLLQQAQGWPEBGMGRTSDSHQWNTLLSLHNAQFDLLQRTPEVARSRAATPLIDLITMA 300
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Qy 301 LTPHPQQAQAVTLPTSVLFIAGHDNTLANLGALIELNMTLPQOPDNTPPGGELVEERW 360
Db 301 LTPHPQQAQAVTLPTSVLFIAGHDNTLANLGALIELNMTLPQOPDNTPPGGELVEERW 360
Qy 361 RRLSDNSQMIQVSLVFQTLQQRDKTPLSLNTPGGEVCLTLAGEBENNAQMGCSLAGFTQ 420
Db 361 RRLSDNSQMIQVSLVFQTLQQRDKTPLSLNTPGGEVCLTLAGEBENNAQMGCSLAGFTQ 420
Qy 421 IYNEARIPACSL 432
Db 421 IYNEARIPACSL 432
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Job time : 89 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Comugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 1, 2004, 21:42:28 ; Search time 531.107 Seconds  
(without alignments)  
1140.289 Million cell updates/sec

Title: US-09-866-379D-9

Perfect score: 1308  
Sequence: 1 atgaagcgatctatccc.....gcagttgagatctatcra 1308

Scoring table: IDENTITY\_NUC  
Gapop 10.0, Gapext 1.0

Searched: 2936184 seqs, 226173202 residues

Total number of hits satisfying chosen parameters: 5872368

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: Published Applications NA:\*  
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3: /cgn2\_6/ptodata/2/pubpna/PTCT\_NEW\_PUB.seq:\*  
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11: /cgn2\_6/ptodata/2/pubpna/US09C\_PUBCOMB.seq:\*  
12: /cgn2\_6/ptodata/2/pubpna/US09\_NEW\_PUB.seq:\*  
13: /cgn2\_6/ptodata/2/pubpna/US09\_NEW\_PUB.seq2:\*  
14: /cgn2\_6/ptodata/2/pubpna/US10\_PUBCOMB.seq:\*  
15: /cgn2\_6/ptodata/2/pubpna/US10\_PUBCOMB.seq2:\*  
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18: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq:\*  
19: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	1308	100.0	1308	15	US-10-156-660-1 Sequence 1, Appl1
2	1265	96.7	1323	9	US-09-777-566A-1 Sequence 1, Appl1
3	1265	96.7	1323	9	US-09-866-379-1 Sequence 1, Appl1
4	1265	96.7	1323	15	US-10-034-985-1 Sequence 1, Appl1
5	1265	96.7	1323	16	US-10-430-356-1 Sequence 1, Appl1
6	1264	96.6	1299	13	US-10-282-122A-7167 Sequence 7167, Ap
7	1263.8	96.6	1299	9	US-09-866-379-6 Sequence 6, Appl1
8	1263.8	96.6	1901	9	US-09-866-379-7 Sequence 7, Appl1
9	1263.8	96.6	1901	15	US-10-156-660-3 Sequence 3, Appl1
10	1262.2	96.5	1901	9	US-09-866-379-5 Sequence 5, Appl1
11	1262.2	96.5	1901	9	US-09-866-379-9 Sequence 9, Appl1
12	1228	93.9	1489	15	US-10-266-041-9 Sequence 9, Appl1
13	1428	93.9	1489	16	US-10-284-962-1 Sequence 1, Appl1
14	1222.4	93.5	1486	16	US-10-284-962-4 Sequence 4, Appl1

15	691.4	52.9	1281	15	US-10-334-672-4 Sequence 4, Appl1
16	691.4	52.9	1281	15	US-10-334-671-4 Sequence 4, Appl1
17	404.8	30.9	466	13	US-10-282-122A-3181 Sequence 3181, Ap
18	230.2	17.6	1326	13	US-10-282-122A-41608 Sequence 41608, A
19	226.2	17.3	1325	15	US-10-021-723A-3 Sequence 3, Appl1
20	223	17.0	1325	15	US-10-021-723A-11 Sequence 11, Appl1
21	212.4	16.2	1325	15	US-10-021-723A-11 Sequence 301, App
22	164.2	12.6	254	16	US-10-317-444-301 Sequence 301, App
23	164.2	12.6	254	16	US-10-317-444-302 Sequence 302, App
24	164.2	12.6	254	16	US-10-317-444-303 Sequence 303, App
25	164.2	12.6	254	16	US-10-317-444-304 Sequence 304, App
26	162.2	12.4	1431	15	US-10-021-723A-9 Sequence 9, Appl1
27	70.8	5.4	1230	15	US-10-021-723A-7 Sequence 7, Appl1
28	62.6	4.8	1266	15	US-10-021-723A-5 Sequence 5, Appl1
29	61	4.7	11710	15	US-10-240-689-40 Sequence 40, Appl1
30	40.4	3.1	427	15	US-10-393-840-372 Sequence 35217, A
31	35.6	2.7	2172	13	US-10-282-122A-35217 Sequence 1364, Ap
32	35.4	2.7	2781	9	US-09-764-847-1364 Sequence 1364, Ap
33	35.4	2.7	2781	15	US-10-092-154-1364 Sequence 1792, Ap
34	35.2	2.7	7164	16	US-10-062-674-1792 Sequence 121, App
35	35	2.7	28729	13	US-10-087-192-121 Sequence 160, App
36	34.4	2.6	392	15	US-10-184-634-160 Sequence 160, App
37	34.4	2.6	392	15	US-10-184-634-312 Sequence 312, App
38	34.2	2.6	802	15	US-10-184-634-312 Sequence 312, App
39	34.2	2.6	802	15	US-10-184-634-312 Sequence 312, App
40	34	2.6	2082	16	US-10-369-493-35563 Sequence 35563, A
41	34	2.6	2879	16	US-10-108-260A-2180 Sequence 2180, Ap
42	33.8	2.6	54	15	US-10-021-723A-47 Sequence 47, Appl1
43	33.8	2.6	1140	16	US-10-369-493-35301 Sequence 35301, A
44	33.8	2.6	1140	16	US-10-369-493-38215 Sequence 38215, A
45	33.8	2.6	1140	16	US-10-369-493-38716 Sequence 38716, A

#### ALIGNMENTS

RESULT 1  
US-10-156-660-1  
Sequence 1, Application US/10156660  
Publication No. US20030103958A1  
GENERAL INFORMATION:  
APPLICANT: Short, Jay M.  
APPLICANT: Kretz, Keith  
APPLICANT: Gray, Kevin A.  
APPLICANT: Barton, Nelson R.  
APPLICANT: Garrett, James B.  
APPLICANT: O'Donoghue, Eileen  
APPLICANT: Mathur, Eric J.  
TITLE OF INVENTION: PHYLASES, NUCLEIC ACIDS ENCODING THEM  
TITLE OF INVENTION: AND METHODS FOR MAKING AND USING THEM  
FILE REFERENCE: 09010-029007  
CURRENT APPLICATION NUMBER: US/10156,660  
CURRENT FILING DATE: 2002-10-01  
PRIOR APPLICATION NUMBER: US 09/866,379  
PRIOR FILING DATE: 2001-05-24  
PRIOR APPLICATION NUMBER: US 09/580,515  
PRIOR FILING DATE: 2000-05-25  
PRIOR APPLICATION NUMBER: US 09/318,528  
PRIOR FILING DATE: 1999-05-25  
PRIOR APPLICATION NUMBER: US 09/291,931  
PRIOR FILING DATE: 1999-04-13  
PRIOR APPLICATION NUMBER: US 09/259,214  
PRIOR FILING DATE: 1999-03-01  
PRIOR APPLICATION NUMBER: US 08/310,798  
PRIOR FILING DATE: 1997-08-13  
NUMBER OF SEQ ID NOS: 4  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 1  
LENGTH: 1308  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: modified phytase enzyme

FEATURE:  
NAME/KEY: CDS  
LOCATION: (1)...(1308)  
US-10-156-660-1

Query Match 100.0%; Score 1308; DB 15; Length 1308;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1308; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 ATGAAAGGATCTTATCCATTTTATCTCTGATCCGTTAACCCCGCATCTGCA 60
DB 1 ATGAAAGGATCTTATCCATTTTATCTCTGATCCGTTAACCCCGCATCTGCA 60
QY 61 TTGCTCAGAGTGAACCCGAGCTGAAGTGAAGTGTGATGTCATGTCATGCT 120
DB 61 TTGCTCAGAGTGAACCCGAGCTGAAGTGAAGTGTGATGTCATGTCATGCT 120
QY 121 GTGCTGCTCCAAACCAAGCCACGCACTGATGCAAGATGTCACCCAGACGCA 180
DB 121 GTGCTGCTCCAAACCAAGCCACGCACTGATGCAAGATGTCACCCAGACGCA 180
QY 181 ACCTGCGCGTAAACCTGGGTGAGTGAACCGCGCGTGGTGAAGCTATGCTAT 240
DB 181 ACCTGCGCGTAAACCTGGGTGAGTGAACCGCGCGTGGTGAAGCTATGCTAT 240
QY 241 GGACATTACTGGGCTCAGGCTGTGAGCCGACGCGATTGCTCTAAATGTGCTGCC 300
DB 241 GGACATTACTGGGCTCAGGCTGTGAGCCGACGCGATTGCTCTAAATGTGCTGCC 300
QY 301 CAGTCTGGTCAAGTGGCATTTATGCTGATGCAACGCGTACCCGTTAAACAGGCGAA 360
DB 301 CAGTCTGGTCAAGTGGCATTTATGCTGATGCAACGCGTACCCGTTAAACAGGCGAA 360
QY 361 GCGTTCGCGCGCGGCGTGGCACTGATGCAATTAACCGTAAATACCCAGGCAATAG 420
DB 361 GCGTTCGCGCGCGGCGTGGCACTGATGCAATTAACCGTAAATACCCAGGCAATAG 420
QY 421 TCCATCCCGATCCGTTATTTAACTGCTTAAACCTGGCGTTGCGCACTGGATTAAC 480
DB 421 TCCATCCCGATCCGTTATTTAACTGCTTAAACCTGGCGTTGCGCACTGGATTAAC 480
QY 481 AACGTGATGACGCGATCTCGAGAGGCGAGAGGTCATTTGCTGATTTACCGGCGAT 540
DB 481 AACGTGATGACGCGATCTCGAGAGGCGAGAGGTCATTTGCTGATTTACCGGCGAT 540
QY 541 TATCAAAAGCGGCTTTCGGAACGTGAACGGGTGCTTAATTTTCGCAATCAACTTGTGC 600
DB 541 TATCAAAAGCGGCTTTCGGAACGTGAACGGGTGCTTAATTTTCGCAATCAACTTGTGC 600
QY 601 CTTAAAGCTGAGAAACAGAGCAAGAGTGTTCATTAACGACGATTCATCGAAATC 660
DB 601 CTTAAAGCTGAGAAACAGAGCAAGAGTGTTCATTAACGACGATTCATCGAAATC 660
QY 661 AAGGTGAGCGCGCATGTGTCTCATTTAACCGTGGGTGAACCTTCGATCTGACG 720
DB 661 AAGGTGAGCGCGCATGTGTCTCATTTAACCGTGGGTGAACCTTCGATCTGACG 720
QY 721 GAGATATTTCTCTCAACAGCAAGAGAAATGCGAGCGCGGAGTGGAGAAAGATCAC 780
DB 721 GAGATATTTCTCTCAACAGCAAGAGAAATGCGAGCGCGGAGTGGAGAAAGATCAC 780
QY 781 GATTCAACCAAGTGAACACTTGTGTAAGTTGCAACGCGCAATTTGATTTGCTCA 840
DB 781 GATTCAACCAAGTGAACACTTGTGTAAGTTGCAACGCGCAATTTGATTTGCTCA 840
QY 841 CGCAGCGCAGAGTGGCGGACGCGCGCAACCCGTTATTAAGTTGATTAAGACGCG 900
DB 841 CGCAGCGCAGAGTGGCGGACGCGCGCAACCCGTTATTAAGTTGATTAAGACGCG 900
QY 901 TTGACGCGCCATTCACCGCAAAACAGGCGTATGATGCAATTAACCATTCAGTGTG 960
DB 901 TTGACGCGCCATTCACCGCAAAACAGGCGTATGATGCAATTAACCATTCAGTGTG 960

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QY 961 TTTATCGCGGACACGATCTATCTGCAAAATCTCGAGCGGCACTGAGCTCACTGG 1020
DB 961 TTTATCGCGGACACGATCTATCTGCAAAATCTCGAGCGGCACTGAGCTCACTGG 1020
QY 1021 AGCGTTCGCGGTACGCGGATTAACGCGCGCGAGTGTGAATCGTGTGTAACGCTGG 1080
DB 1021 AGCGTTCGCGGTACGCGGATTAACGCGCGCGAGTGTGAATCGTGTGTAACGCTGG 1080
QY 1081 CGTGGCTAAGGATTAACGCGAGTGAATTCAGTTGCTGCTGCTTCAGACTTACAG 1140
DB 1081 CGTGGCTAAGGATTAACGCGAGTGAATTCAGTTGCTGCTGCTTCAGACTTACAG 1140
QY 1141 CAGATCGTGAATTAACGCGGCTGTCTTAATTAACGCGCGCGAGAGTGAATCTGAC 1200
DB 1141 CAGATCGTGAATTAACGCGGCTGTCTTAATTAACGCGCGCGAGAGTGAATCTGAC 1200
QY 1201 CTGGCAGATGTAAGAGGAAATGCGCGGCGCATGTGTGCTTGGCAGCTTTACGCA 1260
DB 1201 CTGGCAGATGTAAGAGGAAATGCGCGGCGCATGTGTGCTTGGCAGCTTTACGCA 1260
QY 1261 ATCGTAATGAAGACACGATACCGGCGTGCAGTTGAGATCTCATCTA 1308
DB 1261 ATCGTAATGAAGACACGATACCGGCGTGCAGTTGAGATCTCATCTA 1308

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RESULT 2  
US-09-777-566A-1  
Sequence 1, Application US/0977566A  
Patent No. US20010055789A1

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GENERAL INFORMATION:
APPLICANT: DIVERSA CORPORATION
APPLICANT: SHORT, Jay
APPLICANT: KRETZ, Keith
TITLE OF INVENTION: RECOMBINANT BACTERIAL PHYTASES AND USES THEREOF
FILE REFERENCE: DIVER1370-6
CURRENT APPLICATION NUMBER: US/09/777,566A
CURRENT FILING DATE: 2001-06-11
PRIORITY APPLICATION NUMBER: US 09/318,528
PRIORITY FILING DATE: 1999-05-25
PRIORITY APPLICATION NUMBER: US 09/291,931
PRIORITY FILING DATE: 1999-04-13
PRIORITY APPLICATION NUMBER: US 09/259,214
PRIORITY FILING DATE: 1999-03-01
PRIORITY APPLICATION NUMBER: US 08/910,798
PRIORITY FILING DATE: 1997-08-13
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn version 3.0
SEQ ID NO 1
LENGTH: 1323
TYPE: DNA
ORGANISM: Escherichia coli
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(1320)
NAME/KEY: misc_feature
LOCATION: (1)..(1323)
OTHER INFORMATION: n is any nucleotide
US-09-777-566A-1

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Query Match 96.7%; Score 1265; DB 9; Length 1323;  
Best Local Similarity 98.0%; Pred. No. 0;  
Matches 1280; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

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QY 1 ATGAAAGGATCTTATCCATTTTATCTCTGATCCGTTAACCCCGCATCTGCA 60
DB 1 ATGAAAGGATCTTATCCATTTTATCTCTGATCCGTTAACCCCGCATCTGCA 60
QY 61 TTGCTCAGAGTGAACCCGAGCTGAAGTGAAGTGTGATGTCATGTCATGCT 120
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QY 121 GTGCTGCTCCAAACCAAGCCACGCACTGATGCAAGATGTCACCCAGACGCAATGCGCA 180

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Db 121 GTGGGTGCTCCACCAAGGCCACCACTGATGAGATGTCACCCAGCAGATGCCA 180  
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 Db 181 ACCTGGCCGTAATAACTGGTGAAGTGCACACGGCGGTGGTGAATGATGCTATCTC 240  
 QY 241 GGAATTACTGGCTCAGCGTCTGGTGAAGCCGAGATTGCTGCTTAATGCTGCTCCG 300  
 Db 241 GGAATTACTGGCTCAGCGTCTGGTGAAGCCGAGATTGCTGCTTAATGCTGCTCCG 300  
 QY 301 CAGTCTGGTCAAGTCCGAGTATTGCTGATGTCGACGAGCGGTACCCGTAATAAGCGGAA 360  
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 QY 361 GCTTTCGCGCGCGGTGGTGGCACTGACTGTGCAATTAACCGTATACCCAGCGAGATACG 420  
 Db 361 GCTTTCGCGCGCGGTGGTGGCACTGACTGTGCAATTAACCGTATACCCAGCGAGATACG 420  
 QY 421 TCCAGTCCCGATCCGTTATTTATCTCTAATAAAGTGGCTTGGCACTGGATTAAGCG 480  
 Db 421 TCCAGTCCCGATCCGTTATTTATCTCTAATAAAGTGGCTTGGCACTGGATTAAGCG 480  
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 Db 481 AACGTGACTGACGCGATCTCGAGAGGGCAGAGGGTCAATTGCTGACTTTACCGGGCAT 540  
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 Db 841 CGCAGCGCAGAGGTTGGCGCGAGCGCGCAACCCGTTATTAAGTTGATTAAGAAGCAAGCG 900  
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 QY 1201 CTGGGAGAGATGTGAAGAGCGAAATGCGCAAGGCGATGTGTGTTGGCAGGTTTAAACGCA 1260  
 Db 1201 CTGGGAGAGATGTGAAGAGCGAAATGCGCAAGGCGATGTGTGTTGGCAGGTTTAAACGCA 1260

QY 1261 ATCGTGAATGAAGCAGCATACCGGCGTGCAGATTGAGATCTCATC 1306  
 Db 1261 ATCGTGAATGAAGCAGCATACCGGCGTGCAGATTGAGATCTCATC 1306  
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 ; Sequence 1, Application US/09866379  
 ; Patent No. US20020136754A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: DIVERSA CORPORATION  
 ; APPLICANT: SHORT, Jay  
 ; APPLICANT: KREIZ, Keith  
 ; APPLICANT: GRAY, Kevin  
 ; APPLICANT: BARTON, Nelson  
 ; APPLICANT: GARRETT, James  
 ; APPLICANT: O'DONOGHUE, Eileen  
 ; TITLE OR INVENTION: RECOMBINANT BACTERIAL PHYTASES AND USES THEREOF  
 ; FILE REFERENCE: DIVER1370-7  
 ; CURRENT APPLICATION NUMBER: US/09/866,379  
 ; PRIOR FILING DATE: 2001-05-24  
 ; PRIOR APPLICATION NUMBER: US 09/580,515  
 ; PRIOR FILING DATE: 2000-05-25  
 ; PRIOR APPLICATION NUMBER: US 09/318,528  
 ; PRIOR FILING DATE: 1999-05-25  
 ; PRIOR APPLICATION NUMBER: US 09/291,931  
 ; PRIOR FILING DATE: 1999-04-13  
 ; PRIOR APPLICATION NUMBER: US 09/259,214  
 ; PRIOR FILING DATE: 1999-03-01  
 ; PRIOR APPLICATION NUMBER: US 08/910,798  
 ; PRIOR FILING DATE: 1997-08-13  
 ; NUMBER OF SEQ ID NOS: 10  
 ; SOFTWARE: Patentin version 3.1  
 ; SEQ ID NO 1  
 ; LENGTH: 1323  
 ; TYPE: DNA  
 ; ORGANISM: Escherichia coli  
 ; FEATURE:  
 ; NAME/KEY: misc feature  
 ; LOCATION: (1)..(1323)  
 ; OTHER INFORMATION: n is any nucleotide  
 ; NAME/KEY: CDS  
 ; LOCATION: (1)..(1323)  
 ; OTHER INFORMATION:  
 US-09-866-379-1  
 Query Match 96.7%; Score 1265; DB 9; Length 1323;  
 Best Local Similarity 98.0%; Pred. No. 0;  
 Matches 1280; Conservative 0; Mismatches 26; Indels 0; Gaps 0;  
 QY 1 ATGAAGGATCTTAATCCCATTTTATCTCTGATTCGTTAACCCCGGATCTGCA 60  
 Db 1 ATGAAGGATCTTAATCCCATTTTATCTCTGATTCGTTAACCCCGGATCTGCA 60  
 QY 61 TTGGCTCAAGTGAAGCGCGAGCTGAAGCTGGAAGTGTGTGATTTGCTGCTGCTATGGT 120  
 Db 61 TTGGCTCAAGTGAAGCGCGAGCTGAAGCTGGAAGTGTGTGATTTGCTGCTGCTATGGT 120  
 QY 121 GTGGGTCTCAACCAAGGCCAGCACTGATGACAGATGTCAACCCAGCATGGCCA 180  
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 Db 181 ACCTGGCCGTTAAACTGGGTGAGCTGACACCGCGCGGTGTGAGCTAATGGCTATCTC 240  
 QY 241 GGAATTACTGGGTGAGGCTCTGTAAGCGGAGATGCTGCTTAATGCTGCTCCG 300  
 Db 241 GGAATTACTGGGTGAGGCTCTGTAAGCGGAGATGCTGCTTAATGCTGCTCCG 300  
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Db 301 CAGTCTGTGAGGTCCGATTATTGCTGATGTGACGAGGTACCCGTAACAGGCGAA 360
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Qy 481 AAGTGTACTGACGGGATCTCTGAGAGGGCGAGGGTCAATTGCTGACTTACCGGGCAT 540
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Db 601 CTTTAAACGTGAGAAACAGACGAAAGCTGTTCACTTAACGAGGATTAACATGGAATC 660
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Qy 721 GAGATATTTCTCTGCAACAGCAACAGGAAATCCCGAGCCGGGGTGGGAGATAC 780
Db 721 GAGATATTTCTCTGCAACAGCAACAGGAAATCCCGAGCCGGGGTGGGAGATAC 780
Qy 781 GATTCAACAGCAGTGAACACCTTGTAAATGTTGAATTAAGCGCAATTTGATTGTACAA 840
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Db 841 CGCACGCGCAGAGGTGTCGCCGACGCGGCCACCCCGTTATTGATTTGATCAAGACGCG 900
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Db 1201 CTGCGAGGATGATGAAAGCGAAATGCGAGGGGCAATGATGATGATGATGATGATGATG 1260
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RESULT 4
US-10-034-985-1
; Sequence 1, Application US/10034985
; Publication No. US20030049815A1
; GENERAL INFORMATION:
; APPLICANT: Kretz, Keith

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; TITLE OF INVENTION: NOVEL PHYLASE
; FILE REFERENCE: 09010/029003
; CURRENT APPLICATION NUMBER: US/10/034,985
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: US/09/580,515
; PRIOR FILING DATE: 1999-05-25
; PRIOR APPLICATION NUMBER: 09/291,931
; PRIOR FILING DATE: 1999-04-13
; PRIOR APPLICATION NUMBER: 08/910,798
; PRIOR FILING DATE: 1997-08-13
; PRIOR APPLICATION NUMBER: 09/259,214
; PRIOR FILING DATE: 1999-03-01
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO: 1
; LENGTH: 1323
; TYPE: DNA
; ORGANISM: Escherichia coli
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1320)
; NAME/KEY: misc_feature
; LOCATION: (1)..(1323)
; OTHER INFORMATION: n = A,T,C or G
US-10-034-985-1

Query Match 96.7%; Score 1265; DB 15; Length 1323;
Best Local Similarity 98.0%; Pred. No. 0;
Matches 1280; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

Qy 1 ATGAAAGGATCTTAATCCATTTTATCTCTTGTGATTCGATTAACCCGCAATCTGCA 60
Db 1 ATGAAAGGATCTTAATCCATTTTATCTCTTGTGATTCGATTAACCCGCAATCTGCA 60
Qy 61 TTGCTGAGATGAGCCGAGCTGAAAGTGTGATGATGATGATGATGATGATGATGATG 120
Db 61 TTGCTGAGATGAGCCGAGCTGAAAGTGTGATGATGATGATGATGATGATGATGATG 120
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Db 121 GTGCGTGTCCACCAAGGACGACGCACTGATGAGATGCAACCCAGAGCATGAGCA 180
Qy 181 AACTGCGCGGTAACCTGAGTGAACACGCGCGCGGTGATGATGATGATGATGATG 240
Db 181 AACTGCGCGGTAACCTGAGTGAACACGCGCGCGGTGATGATGATGATGATGATG 240
Qy 181 AACTGCGCGGTAACCTGAGTGAACACGCGCGCGGTGATGATGATGATGATGATG 240
Db 181 AACTGCGCGGTAACCTGAGTGAACACGCGCGCGGTGATGATGATGATGATGATG 240
Qy 241 GGAACAATTACGCGCAGCGCTGAGTGAACGAGATGCTGCTAAATGAGCTGCGCG 300
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Qy 241 GGAACAATTACGCGCAGCGCTGAGTGAACGAGATGCTGCTAAATGAGCTGCGCG 300
Db 241 GGAACAATTACGCGCAGCGCTGAGTGAACGAGATGCTGCTAAATGAGCTGCGCG 300
Qy 301 CAGTCTGTGAGGTGCGGATTAATGCTGATGATGATGATGATGATGATGATGATG 360
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Qy 601 CTTTAAACGTGAGAAACAGACGAAAGCTGTTCACTTAACGAGGATTAACATGGAATC 660
Db 601 CTTTAAACGTGAGAAACAGACGAAAGCTGTTCACTTAACGAGGATTAACATGGAATC 660

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Qy 661 AAGGTAGCCGCGAAGTGTCTCTAATTAACCGGTGCGTAAGCTTCGATCAATGCTGACG 720
Db 661 AAGGTAGCCGCGAAGTGTCTCTAATTAACCGGTGCGTAAGCTTCGATCAATGCTGACG 720
Qy 721 GAGATATTTCTCTGCAACAGCAACAGGGAATGCGAGCGGGGTGGGGAAGATCACC 780
Db 721 GAGATATTTCTCTGCAACAGCAACAGGGAATGCGAGCGGGGTGGGGAAGATCACC 780
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Db 781 GATTCAACACAGTGAACACCTTGCTAATGTTGCAATACCGGCAATTTGATTGCTACAA 840
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Db 841 CGCAGCCGAGAGTTGGCCCGGAGCGCGCCACCCCGTATTAAGTTGATCAACAGCG 900
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Db 1201 CTGGCAGAGTGTGAAGAGCGAATGCGCAGGCAATGTTGCTTGCGCAGTTTACGAA 1260
Qy 1261 ATCGGATGAAGCAACGATACCGGCTGCAAGTTGAGATCTCATC 1306
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## RESULT 5

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US-10-430-356-1
; Sequence 1, Application US/10430356
; Publication No. US20030232041A1
; GENERAL INFORMATION:
; APPLICANT: Kretz, Keith
; TITLE OF INVENTION: NOVEL PHYTASE
; FILE REFERENCE: 09010/029003
; CURRENT APPLICATION NUMBER: US/10/430,356
; CURRENT FILING DATE: 2003-05-05
; PRIOR APPLICATION NUMBER: US/09/580,515
; PRIOR FILING DATE: 1999-05-25
; PRIOR APPLICATION NUMBER: 09/318,528
; PRIOR FILING DATE: 1999-05-25
; PRIOR APPLICATION NUMBER: 09/291,931
; PRIOR FILING DATE: 1999-04-13
; PRIOR APPLICATION NUMBER: 08/910,798
; PRIOR FILING DATE: 1997-08-13
; PRIOR APPLICATION NUMBER: 09/259,214
; PRIOR FILING DATE: 1999-03-01
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1323
; TYPE: DNA
; ORGANISM: Escherichia coli
; FEATURE:

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; NAME/KEY: CDS
; LOCATION: (1)...(1320)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(1323)
; OTHER INFORMATION: n = A,T,C or G
US-10-430-356-1

Query Match      96.7%; Score 1265; DB 16; Length 1323;
Best Local Similarity 98.0%; Pred. No. 0; Mismatches 26; Indels 0; Gaps 0;
Matches 1280; Conservative 0;

Qy 1 ATGAAGCATCTTAATCCATTTTATCTCTTGATTCGTTAACCAGCATCTGCA 60
Db 1 ATGAAGCATCTTAATCCATTTTATCTCTTGATTCGTTAACCAGCATCTGCA 60
Qy 61 TTGCTCAAGTGAAGCCGGAAGCTGAAGCTGAAGAGTGTGATGTTGATGCTATG 120
Db 61 TTGCTCAAGTGAAGCCGGAAGCTGAAGAGTGTGATGTTGATGCTATG 120
Qy 121 GTGCGTCTCAACCAAGGCGACGCAACTGATGCAAGATGTCACCCAGCATGCGCA 180
Db 121 GTGCGTCTCAACCAAGGCGACGCAACTGATGCAAGATGTCACCCAGCATGCGCA 180
Qy 181 ACCTGCGCGTAAACTGGGTGAGCTGACACCGCGGTGTGAGCTTAATGCTATCTC 240
Db 181 ACCTGCGCGTAAACTGGGTGAGCTGACACCGCGGTGTGAGCTTAATGCTATCTC 240
Qy 241 GGAATTAATGCGCTCAAGGCTCTGTTAGCCGAGATGCTGCTTAATGTTGCTGCGG 300
Db 241 GGAATTAATGCGCTCAAGGCTCTGTTAGCCGAGATGCTGCTTAATGTTGCTGCGG 300
Qy 301 CAGTGTGTCAGGTGCGGATTAATGCTGATGTCGACAGCTGATACCGTAAACAGCGCA 360
Db 301 CAGTGTGTCAGGTGCGGATTAATGCTGATGTCGACAGCTGATACCGTAAACAGCGCA 360
Qy 361 GCTTTGCGCGCGGCTGGCACTGACTGTGCAATACCTGATACAGGCAATACG 420
Db 361 GCTTTGCGCGCGGCTGGCACTGACTGTGCAATACCTGATACAGGCAATACG 420
Qy 421 TCCAGTCCCGATCCGTTATTTATCTCTAATAAACTGGGTTTGGCACTGATTAACG 480
Db 421 TCCAGTCCCGATCCGTTATTTATCTCTAATAAACTGGGTTTGGCACTGATTAACG 480
Qy 481 AACGTATGACGCGATCTCTGAGAGGCGAGAGGTCATTGCTGACTTTACGGGCAT 540
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Db 541 TATCAACCGCGCTTGGCGAATGGAACGGGTGCTTAATTTTCGCAATCAACTGTG 600
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Db 601 CTTAAACGTGAAGAACAGACGAAAGCTGTTCAATTAACGAGGCAATTAACATGGAATC 660
Qy 661 AAGTGAAGCGCGACGCTGCTCAATTAACGCGGTGAAGCTGCAATCAATGCTGAG 720
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Db 721 GAGATATTTCTCTGCAACAGCAACAGGGAATGCGAGCGGGGTGGGGAAGATCACC 780
Qy 781 GATTCAACACAGTGAACACCTTGCTAATGTTGCAATACCGGCAATTTGATTGCTACAA 840
Db 781 GATTCAACACAGTGAACACCTTGCTAATGTTGCAATACCGGCAATTTGATTGCTACAA 840
Qy 841 CGCAGCCGAGAGTTGGCCCGGAGCGCGCCACCCCGTATTAAGTTGATCAACAGCG 900
Db 841 CGCAGCCGAGAGTTGGCCCGGAGCGCGCCACCCCGTATTAAGTTGATCAACAGCG 900
Qy 901 TTGACGCCCATCCACCGCAAAAACAGCGCTATGTTGATTAACCACTTCAGTCTG 960

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Db	901	TTGACGCCCATCCACCGCAAAAACAGCCGATGCTGTGACATTACCACTTCAGTACTG	960
QY	961	TTTATCGCCGACACGACTACTTAATCTGGCAATCTCGCGCCGACCTGGAGCTCAACTGG	1020
Db	961	TTTATTTCCCGACACGATACTTAATCTGGCAATCTCGCGCCGACCTGGAGCTCAACTGG	1020
QY	1021	ACGCTTCCCGGTCAGCCGCGATACACGCGCCGACAGTGGTGAACCTGATTTTGAACGCTGG	1080
Db	1021	ACGCTTTCCCGGTCAGCCGCGATACACGCGCCGACAGTGGTGAACCTGATTTTGAACGCTGG	1080
QY	1081	CGTGGCTTACGCGATTACACGCCAGTGGATTCAAGTTTCGTGCTTTCAGACTTTACAG	1140
Db	1081	CGTGGCTTACGCGATTACACGCCAGTGGATTCAAGTTTCGTGCTTTCAGACTTTACAG	1140
QY	1141	CAGATGCGGTGATTAACAGCGCGCTGCATTAATAACGCCGCCCGAGAGAGGTAACTGACC	1200
Db	1141	CAGATGCGGTGATTAACAGCGCGCTGCATTAATAACGCCGCCCGAGAGAGGTAACTGACC	1200
QY	1201	CTGGCAGGATGTGAAGAGCGAATGCGCAGGCGCATGTGTGCTTGGCAGTTTTACGCA	1260
Db	1201	CTGGCAGGATGTGAAGAGCGAATGCGCAGGCGCATGTGTGCTTGGCAGTTTTACGCA	1260
QY	1261	ATCGTGATGAAGACACGCAATCCCGCGCGACAGTTGAGATCTCAATC	1306
Db	1261	ATCGTGATGAAGACACGCAATCCCGCGCGACAGTTGAGATCTCAATC	1306

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RESULT 6
US-10-282-122A-7167
: Sequence 7167, Application US/10282122A
: Publication No. US20040029122A1
GENERAL INFORMATION:
APPLICANT: Wang, Hiansu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Carr, Grant
APPLICANT: Yamamoto, Robert
APPLICANT: Forsyth, R.
APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: EDI TRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIORITY APPLICATION NUMBER: 60/191,078
PRIORITY FILING DATE: 2000-03-21
PRIORITY APPLICATION NUMBER: 60/206,848
PRIORITY FILING DATE: 2000-05-23
PRIORITY APPLICATION NUMBER: 60/207,727
PRIORITY FILING DATE: 2000-05-26
PRIORITY APPLICATION NUMBER: 60/230,335
PRIORITY FILING DATE: 2000-09-06
PRIORITY APPLICATION NUMBER: 60/230,347
PRIORITY FILING DATE: 2000-09-09
PRIORITY APPLICATION NUMBER: 60/242,578
PRIORITY FILING DATE: 2000-10-23
PRIORITY APPLICATION NUMBER: 60/253,625
PRIORITY FILING DATE: 2000-11-27
PRIORITY APPLICATION NUMBER: 60/257,931
PRIORITY FILING DATE: 2000-12-22
PRIORITY APPLICATION NUMBER: 60/267,636
PRIORITY FILING DATE: 2001-02-09
PRIORITY APPLICATION NUMBER: 60/269,308
PRIORITY FILING DATE: 2001-02-16
Remaining Priority Application data removed - See File Wrapper or PAM.
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
: SEQ ID NO 7167

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Query Match	96.6%	Score 1264	DB 13	Length 1299
Best Local Similarity	98.5%	Pred. No. 0		
Matches 1276	Conservative 0	Mismatches 20	Indels 0	Gaps 0
<p>Organism: <i>Escherichia coli</i></p> <p>Query-1282-122A-7167</p>				
1	ATGAAAGCATCTTATCCCATTTTATCTCTTCTGATCCGTTAAACCCCGCATCTGCA	60		
1	ATGAAAGCATCTTATCCCATTTTATCTCTTCTGATCCGTTAAACCCCGCATCTGCA	60		
61	TTGCGTCAGAGTGAAGCCGAGCTGAAGTGTGATGTCACTGCTCACTGCT	120		
61	TTGCGTCAGAGTGAAGCCGAGCTGAAGTGTGATGTCACTGCTCACTGCT	120		
121	GTGCGGTCTCCACCAAGGCCACGAACTGATGTGAGAGATGCAACCCGACGATGCCA	180		
121	GTGCGGTCTCCACCAAGGCCACGAACTGATGTGAGAGATGCAACCCGACGATGCCA	180		
181	ACCTGGCCGGTAAATCTGGTGAAGTGAACACCGCGCGTGTGATGCTTATCTC	240		
181	ACCTGGCCGGTAAATCTGGTGAAGTGAACACCGCGCGTGTGATGCTTATCTC	240		
241	GGAATTATGCGGTCAACGCTGCTGGTACCGGATTTGCTGCTAAATGTGCTGACCG	300		
241	GGAATTATGCGGTCAACGCTGCTGGTACCGGATTTGCTGCTAAATGTGCTGACCG	300		
301	CAGTCTGTCAAGTGCAGATTAATGCTGATGTGACGAGGTACCGGTAAACAGGCGAA	360		
301	CAGTCTGTCAAGTGCAGATTAATGCTGATGTGACGAGGTACCGGTAAACAGGCGAA	360		
361	GCTTTGCGCGCGGGGTGACACTGACCTGACCTGACCTGACCTGACCTGACCTGAC	420		
361	GCTTTGCGCGCGGGGTGACACTGACCTGACCTGACCTGACCTGACCTGACCTGAC	420		
421	TCCAGTCCCGATCCGTTATTTATCTCTTAAATCTGCGTTTGCACCTGTATTAACCG	480		
421	TCCAGTCCCGATCCGTTATTTATCTCTTAAATCTGCGTTTGCACCTGTATTAACCG	480		
481	AACGTGATGACCGCATCTCGAGAGGCGAGAGGATCAATGCTGATTTACCGGGCAT	540		
481	AACGTGATGACCGCATCTCGAGAGGCGAGAGGATCAATGCTGATTTACCGGGCAT	540		
541	TATCAAAACGCGTTTGCAGACTGGAAGGCGTGTATTTTTCGCAATCAACTGTGTC	600		
541	TATCAAAACGCGTTTGCAGACTGGAAGGCGTGTATTTTTCGCAATCAACTGTGTC	600		
601	CTTAAACGTGAAGAACAGAGCAAAAGCTGTTCAATTAACGAGGATTAACATGCGAATC	660		
601	CTTAAACGTGAAGAACAGAGCAAAAGCTGTTCAATTAACGAGGATTAACATGCGAATC	660		
661	AAGGTAGCGCGCATGCTGCTCAATTAACGAGTGCAGTAAAGCTCGCATCAATGCTGACG	720		
661	AAGGTAGCGCGCATGCTGCTCAATTAACGAGTGCAGTAAAGCTCGCATCAATGCTGACG	720		
721	GAGATATTTCTCTGCAACAGACAGAGAAATGCCGAGCCGCGGTGTGGGAAGATATAC	780		
721	GAGATATTTCTCTGCAACAGACAGAGAAATGCCGAGCCGCGGTGTGGGAAGATATAC	780		
781	GATTCACACAGAGGAAACCTTGTAGTTGCAATAAGCGCAATTTATTTTGCTACAA	840		
781	GATTCACACAGAGGAAACCTTGTAGTTGCAATAAGCGCAATTTATTTTGCTACAA	840		
841	CGACGCGCAGAGTTCGCGCAGCCGCGCACCCCGTATTAGATTGATCAAGACAGCG	900		
841	CGACGCGCAGAGTTCGCGCAGCCGCGCACCCCGTATTAGATTGATCAAGACAGCG	900		
901	TTGAGCGCCCATCAACGCAAAACAGAGGTATGAGTGTGACATTAACCATTTAGTGTG	960		
901	TTGAGCGCCCATCAACGCAAAACAGAGGTATGAGTGTGACATTAACCATTTAGTGTG	960		
960	TTGAGCGCCCATCAACGCAAAACAGAGGTATGAGTGTGACATTAACCATTTAGTGTG	960		

Qy 961 TTTATCCCGGACACGATCTACTAATCTGCAATCTCGCGCGACATGAGCTCAACTG 1020  
Db 961 TTTATCCCGGACACGATCTACTAATCTGCAATCTCGCGCGCGACATGAGCTCAACTG 1020  
Qy 1021 ACGCTTCCCGGACACGCGGATTAACACCGCGGAGTGTGAACGTGTGTTGAACGTG 1080  
Db 1021 ACGCTTCCCGGACACGCGGATTAACACCGCGGAGTGTGAACGTGTGTTGAACGTG 1080  
Qy 1081 CGTGGCGGATTAACACGCGGATTAACACCGCGGAGTGTGAACGTGTGTTGAACGTG 1140  
Db 1081 CGTGGCGGATTAACACGCGGATTAACACCGCGGAGTGTGAACGTGTGTTGAACGTG 1140  
Qy 1141 CAGATGCGGATTAACACCGCGGATTAACACCGCGGAGTGTGAACGTGTGTTGAACGTG 1200  
Db 1141 CAGATGCGGATTAACACCGCGGATTAACACCGCGGAGTGTGAACGTGTGTTGAACGTG 1200  
Qy 1201 CTGGCAGGATTAACACGCGGATTAACACCGCGGAGTGTGAACGTGTGTTGAACGTG 1260  
Db 1201 CTGGCAGGATTAACACGCGGATTAACACCGCGGAGTGTGAACGTGTGTTGAACGTG 1260  
Qy 1261 ATCGGATTAACACGCGGATTAACACCGCGGAGTGTGAACGTGTGTTGAACGTG 1296  
Db 1261 ATCGGATTAACACGCGGATTAACACCGCGGAGTGTGAACGTGTGTTGAACGTG 1296

RESULT 7  
US-09-866-379-6  
Sequence 6, Application US/09866379  
Patent No. US20020136754A1  
GENERAL INFORMATION:  
APPLICANT: DIVERSA CORPORATION.  
APPLICANT: SHORT, Jay  
APPLICANT: KRETZ, Keith  
APPLICANT: GRAY, Kevin  
APPLICANT: BARTON, Nelson  
APPLICANT: GARRETT, James  
APPLICANT: O'DONOGHUE, Eileen  
TITLE OF INVENTION: RECOMBINANT BACTERIAL PHYTASES AND USES THEREOF  
FILE REFERENCE: DIVER1370-7  
CURRENT APPLICATION NUMBER: US/09/866,379  
CURRENT FILING DATE: 2001-05-24  
PRIOR APPLICATION NUMBER: US 09/580,515  
PRIOR FILING DATE: 2000-05-25  
PRIOR APPLICATION NUMBER: US 09/318,528  
PRIOR FILING DATE: 1999-05-25  
PRIOR APPLICATION NUMBER: US 09/291,931  
PRIOR FILING DATE: 1998-04-13  
PRIOR APPLICATION NUMBER: US 09/259,214  
PRIOR FILING DATE: 1999-03-01  
PRIOR APPLICATION NUMBER: US 08/910,798  
PRIOR FILING DATE: 1997-08-13  
NUMBER OF SEQ ID NOS: 10  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 6  
LENGTH: 1901  
TYPE: DNA  
ORGANISM: Escherichia coli  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (1)-(1901)  
OTHER INFORMATION: n is any nucleotide  
US-09-866-379-6

Query Match 96.6%; Score 1263.8; DB 9; Length 1901;  
Best Local Similarity 98.2%; Pred. No. 0;  
Matches 1277; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

Qy 1 AAGGAAGCGATCTGATCCATTTTATCTCTGATTCGCTTAACCCCGCAATCTCA 60  
Db 188 AAGGAAGCGATCTGATCCATTTTATCTCTGATTCGCTTAACCCCGCAATCTCA 247  
Qy 61 TTGCTCAGAGTGAAGCGGAGCTGAAGCTGAAGTGTGTGATTTGTCACTGATGAT 120

Db 248 TTGCTCAGAGTGAAGCGGAGCTGAAGCTGAAGTGTGTGATTTGTCACTGATGAT 307  
Qy 121 GTGCTGCTCAACCAAGGCGACGCACTGATGCAAGATGTCAACCCAGACGATGCGCA 180  
Db 308 GTGCTGCTCAACCAAGGCGACGCACTGATGCAAGATGTCAACCCAGACGATGCGCA 367  
Qy 181 ACGTGGCGGATTAACCTGGGTGAGCTGAACACCGCGGAGTGTGAACGTGTGTTGAACGTG 240  
Db 368 ACGTGGCGGATTAACCTGGGTGAGCTGAACACCGCGGAGTGTGAACGTGTGTTGAACGTG 427  
Qy 241 GGAATTAATGCGGCTGAGGCTGTGGTAGCCGACGATGCTGCTTAATGTGTGCTGCCG 300  
Db 428 GGAATTAATGCGGCTGAGGCTGTGGTAGCCGACGATGCTGCTTAATGTGTGCTGCCG 487  
Qy 301 CAGTGTGCTGAGTGTGCGATTTATGCTGATGTGACGACGATGCTGCTTAATGTGTGCTGCCG 360  
Db 488 CAGTGTGCTGAGTGTGCGATTTATGCTGATGTGACGACGATGCTGCTTAATGTGTGCTGCCG 547  
Qy 361 GCTTGGCGGCGGAGTGTGCACTGATGCTGCAATTAACGATACCAAGGAGATGACG 420  
Db 548 GCTTGGCGGCGGAGTGTGCACTGATGCTGCAATTAACGATACCAAGGAGATGACG 607  
Qy 421 TCCAGTCCCGATCCGTTATTTAATCTTAAACTGCGCTTTGCCAATGAGTAAACCGG 480  
Db 608 TCCAGTCCCGATCCGTTATTTAATCTTAAACTGCGCTTTGCCAATGAGTAAACCGG 667  
Qy 481 AAGTGAATCGAGCGGATCTCTGAGAGGAGGAGGATCAATGCTGATTAACCGGAGAT 540  
Db 668 AAGTGAATCGAGCGGATCTCTGAGAGGAGGAGGATCAATGCTGATTAACCGGAGAT 727  
Qy 541 TATCAACGCGGCTTTGCGCACTGAAACGCGGTCTTAATTTTCCGCAATGAAACTTGTGC 600  
Db 728 CGGCAACGCGGCTTTGCGCACTGAAACGCGGTCTTAATTTTCCGCAATGAAACTTGTGC 787  
Qy 601 CTTAAACGTAAGAAACAGACCAAGACGCTGTCAATTAACGACGATTAACCGGAGAT 660  
Db 788 CTTAAACGTAAGAAACAGACCAAGACGCTGTCAATTAACGACGATTAACCGGAGAT 847  
Qy 661 AAGTGAATCGAGCGGATCTCTGAGAGGAGGAGGATCAATGCTGATTAACCGGAGAT 720  
Db 848 AAGTGAATCGAGCGGATCTCTGAGAGGAGGAGGATCAATGCTGATTAACCGGAGAT 907  
Qy 721 GAGATATTTCTCTGCAACAGACAGGAAATGCGGAGCGGAGTGTGAGAAAGATCAAC 780  
Db 908 GAGATATTTCTCTGCAACAGACAGGAAATGCGGAGCGGAGTGTGAGAAAGATCAAC 967  
Qy 781 GATTCAACAGGAGAAACCTGTGATTAACCGGTGCGGTAAAGCTGCAATGCTGACG 840  
Db 968 GATTCAACAGGAGAAACCTGTGATTAACCGGTGCGGTAAAGCTGCAATGCTGACG 1027  
Qy 841 CGCAAGCGAGAGGTTCCCGGACGCGGCGCAACCCCGTTATTAATTTGATTAACAGACG 900  
Db 1028 CGCAAGCGAGAGGTTCCCGGACGCGGCGCAACCCCGTTATTAATTTGATTAACAGACG 1087  
Qy 901 TTGAAGCGGATTAACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 960  
Db 1088 TTGAAGCGGATTAACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1147  
Qy 961 TTTATCCCGGACACGATCTACTAATCTGCAATCTCGCGCGCGACATGAGCTCAACTG 1020  
Db 1148 TTTATCCCGGACACGATCTACTAATCTGCAATCTCGCGCGCGACATGAGCTCAACTG 1207  
Qy 1021 ACGCTTCCCGGACACGCGGATTAACACCGCGGAGTGTGAACGTGTGTTGAACGTG 1080  
Db 1208 ACGCTTCCCGGACACGCGGATTAACACCGCGGAGTGTGAACGTGTGTTGAACGTG 1267  
Qy 1081 CGTGGCGGATTAACACGCGGATTAACACCGCGGAGTGTGAACGTGTGTTGAACGTG 1140  
Db 1268 CGTGGCGGATTAACACGCGGATTAACACCGCGGAGTGTGAACGTGTGTTGAACGTG 1327  
Qy 1141 CAGATGCGGATTAACACGCGGATTAACACCGCGGAGTGTGAACGTGTGTTGAACGTG 1200  
Db 1328 CAGATGCGGATTAACACGCGGATTAACACCGCGGAGTGTGAACGTGTGTTGAACGTG 1387

QY 1201 CTGGCAGAGATGTGAAGAGCGAATGCCAGAGCATGTGTTGTCGACAGTTTACGAA 1260  
DB 1388 CTGGCAGAGATGTGAAGAGCGAATGCCAGAGCATGTGTTGTCGACAGTTTACGAA 1447  
QY 1261 ATCGTGAATGAGACGACATACCGCGCTGACAGTTTGAGAT 1300  
DB 1448 ATCGTGAATGAGACGACATACCGCGCTGACAGTTTGAT 1487

RESULT 8  
US-09-866-379-7  
Sequence 7, Application US/09866379  
Patent No. US20020136754A1  
GENERAL INFORMATION:

APPLICANT: DIVERSA CORPORATION  
APPLICANT: SHORT, Jay  
APPLICANT: KRETZ, Keith  
APPLICANT: GRAY, Kevin  
APPLICANT: BARTON, Nelson  
APPLICANT: GARRETT, James  
APPLICANT: O'DONOGHUE, Eileen  
TITLE OF INVENTION: RECOMBINANT BACTERIAL PHOSPHATASES AND USES THEREOF  
FILE REFERENCE: DIVER370-7  
CURRENT APPLICATION NUMBER: US/09/866,379  
PRIOR APPLICATION NUMBER: US 09/580,515  
PRIOR FILING DATE: 2001-05-24  
PRIOR APPLICATION NUMBER: US 09/318,528  
PRIOR FILING DATE: 1999-05-25  
PRIOR APPLICATION NUMBER: US 09/291,931  
PRIOR FILING DATE: 1999-04-13  
PRIOR APPLICATION NUMBER: US 09/259,214  
PRIOR FILING DATE: 1999-03-01  
PRIOR APPLICATION NUMBER: US 08/910,798  
PRIOR FILING DATE: 1997-08-13  
NUMBER OF SEQ ID NOS: 10  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 7  
LENGTH: 1901  
TYPE: DNA  
ORGANISM: Escherichia coli  
FEATURES:  
NAME/KEY: misc feature  
LOCATION: (1)..(1901)  
OTHER INFORMATION: n is any nucleotide  
US-09-866-379-7

Query Match 96.6%; Score 1263.8; DB 9; Length 1901;  
Best Local Similarity 98.2%; Pred. No. 0;  
Matches 1277; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

QY 1 ATGAAAGCATCTTAATCCATTTTATCTTTGATTCGCTTAACCCCGCATCTGCA 60  
DB 188 ATGAAAGCATCTTAATCCATTTTATCTTTGATTCGCTTAACCCCGCATCTGCA 247  
QY 61 TTGCGTCAGAGTAGAGCCGAGCTGAAGCTGGAAGTGTGATTTGTCAGTCTGATGAT 120  
DB 248 TTGCGTCAGAGTAGAGCCGAGCTGAAGCTGGAAGTGTGATTTGTCAGTCTGATGAT 307  
QY 121 GTGCGTCTCCAAACCAAGCCACGCACTGATGACGATGTCACCCCAAGCATGGCCA 180  
DB 308 GTGCGTCTCCAAACCAAGCCACGCACTGATGACGATGTCACCCCAAGCATGGCCA 367  
QY 181 ACCTGCGCGGTAAACCTGGGTGAGCTGACACCGCGGTGATGACTAATGCGCTATCTC 240  
DB 368 ACCTGCGCGGTAAACCTGGGTGAGCTGACACCGCGGTGATGACTAATGCGCTATCTC 427  
QY 241 GGACATTAATGCGGTGACGCTGCTGAGCCGACGAGATTGCTGCTAAATGTGCTGCCG 300  
DB 428 GGACATTAATGCGGTGACGCTGCTGAGCCGACGAGATTGCTGCTGCAAAAAGGCTGCCG 487  
QY 301 CAGTCTGCTGAGGTGCGATTAATGCTGATGTGACGAGCGTACCCTAAACAGGCGAA 360

DB 488 CAGTCTGCTGAGGTGCGATTAATGCTGATGTGACGAGCGTACCCTAAACAGGCGAA 547  
QY 361 GCCTTCGCGCGCGGCTGGACCTGACTGTGCAATACCGTACATACCCAGGAGATACG 420  
DB 548 GCCTTCGCGCGCGGCTGGACCTGACTGTGCAATACCGTACATACCCAGGAGATACG 607  
QY 421 TCCAGTCCCGAATCCGATTAATCTCTTAAATACTGCGCTTGGCCAACTGATTAACGCG 480  
DB 608 TCCAGTCCCGAATCCGATTAATCTCTTAAATACTGCGCTTGGCCAACTGATTAACGCG 667  
QY 481 AACGTACTGACGCGATCTCTGAAAGGCGAGAGGTCATTTGCTGACTTTACCGGCGAT 540  
DB 668 AACGTACTGACGCGATCTCTGAAAGGCGAGAGGTCATTTGCTGACTTTACCGGCGAT 727  
QY 541 TATCAACGCGGCTTCGGAACCTGAAACGCGGTGCTTAATTTCCGCAATCAACTGTGC 600  
DB 728 CCGCAACGCGGCTTCGGAACCTGAAACGCGGTGCTTAATTTCCGCAATCAACTGTGC 787  
QY 601 CTTAAACGTGAGAAACAGAGCGAAAGCTGTCATTAAACGAGCATTAACATTCGAACTC 660  
DB 788 CTTAAACGTGAGAAACAGAGCGAAAGCTGTCATTAAACGAGCATTAACATTCGAACTC 847  
QY 661 AAGTGAGCGCGGATGTGCTCATTTAACGCGGTGCGTACGATCAATGCTGACG 720  
DB 848 AAGTGAGCGCGGATGTGCTCATTTAACGCGGTGCGTACGATCAATGCTGACG 907  
QY 721 GAGATATTTCTCTGCAACAGCAACGGAATGCCGAGCCGCGGTGGGAAAGATCAC 780  
DB 908 GAGATATTTCTCTGCAACAGCAACGGAATGCCGAGCCGCGGTGGGAAAGATCAC 967  
QY 781 GATTACACCGATGGAACACCTGTAGTTGCAATACGCGCAATTGATTTGCTACAA 840  
DB 968 GATTACACCGATGGAACACCTGTAGTTGCAATACGCGCAATTGATTTGCTACAA 1027  
QY 841 CCGACGCGAGAGTGTCCCGGAGCCGCGCAACCCGTTATTAGATTGATCAAGACGCG 900  
DB 1028 CCGACGCGAGAGTGTCCCGGAGCCGCGCAACCCGTTATTAGATTGATCAAGACGCG 1087  
QY 901 TTGAGCGCCCATCCACCGCAAAAACAGCGGTATGTGTGATTAACCATTCAGTGTG 960  
DB 1088 TTGAGCGCCCATCCACCGCAAAAACAGCGGTATGTGTGATTAACCATTCAGTGTG 1147  
QY 961 TTTATCGCGGACACGATTAATCTGCAATCTGCGCGGCGCACTGAGCTCAACTGCG 1020  
DB 1148 TTTATCGCGGACACGATTAATCTGCAATCTGCGCGGCGCACTGAGCTCAACTGCG 1207  
QY 1021 AGGCTTCCCGTCAAGCCGATTAACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1080  
DB 1208 AGGCTTCCCGTCAAGCCGATTAACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1267  
QY 1081 CGTGGCTAAGCGATTAACG 1140  
DB 1268 CGTGGCTAAGCGATTAACG 1327  
QY 1141 CAGATCGGTATTAACG 1200  
DB 1328 CAGATCGGTATTAACG 1387  
QY 1201 CTGGCAGAGTAGAGAGGAAATGCGAGGCGATGTGTTGCTTGGAGGTTTACGCA 1260  
DB 1388 CTGGCAGAGTAGAGAGGAAATGCGAGGCGATGTGTTGCTTGGAGGTTTACGCA 1447  
QY 1261 ATCGTGAATGAGACGACATACCGCGGTGACAGTTTGAGAT 1300  
DB 1448 ATCGTGAATGAGACGACATACCGCGGTGACAGTTTGAT 1487

RESULT 9  
US-10-156-660-3  
Sequence 3, Application US/10156660  
Publication No. US20030103958A1  
GENERAL INFORMATION:

```

/ APPLICANT: Short, Jay M.
/ APPLICANT: Kretz, Keith
/ APPLICANT: Gray, Kevin A.
/ APPLICANT: Barton, Nelson R.
/ APPLICANT: Garrett, James B.
/ APPLICANT: O'Donoghue, Eileen
/ APPLICANT: Mathur, Eric J.
/ TITLE OF INVENTION: PHYTASES, NUCLEIC ACIDS ENCODING THEM
/ TITLE OF INVENTION: AND METHODS FOR MAKING AND USING THEM
/ FILE REFERENCE: 0910-029007
/ CURRENT APPLICATION NUMBER: US/10/156,660
/ CURRENT FILING DATE: 2002-10-01
/ PRIOR APPLICATION NUMBER: US 09/866,379
/ PRIOR FILING DATE: 2001-05-24
/ PRIOR APPLICATION NUMBER: US 09/580,515
/ PRIOR FILING DATE: 2000-05-25
/ PRIOR APPLICATION NUMBER: US 09/318,528
/ PRIOR FILING DATE: 1999-05-25
/ PRIOR APPLICATION NUMBER: US 09/291,931
/ PRIOR FILING DATE: 1999-04-13
/ PRIOR APPLICATION NUMBER: US 09/259,214
/ PRIOR FILING DATE: 1999-03-01
/ PRIOR APPLICATION NUMBER: US 08/910,798
/ PRIOR FILING DATE: 1997-08-13
/ NUMBER OF SEQ ID NOS: 4
/ SOFTWARE: FASTSEQ for Windows Version 4.0
/ SEQ ID NO 3
/ LENGTH: 1901
/ TYPE: DNA
/ ORGANISM: Escherichia coli
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (188)...(1483)
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: 403
/ OTHER INFORMATION: n = A,T,C or G
US-10-156-660-3

Query Match      96.6%; Score 1263.8; DB 15; Length 1901;
Best Local Similarity 98.2%; Pred. No. 0;
Matches 1277; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

Cy 1 ATGAAGCGATCTTAATCCCATTTTATCTTCTGATTCGGTTAACCCGCAATCGCA 60
Db 188 ATGAAGCGATCTTAATCCCATTTTATCTTCTGATTCGGTTAACCCGCAATCGCA 247
Cy 61 TTCCTCAAGTGAAGCCGAGCTGAAGCTGAAGAGTGTGATTTGTCATGTCATGTC 120
Db 248 TTCCTCAAGTGAAGCCGAGCTGAAGCTGAAGAGTGTGATTTGTCATGTCATGTC 307
Cy 121 GTGGGTGCTCAACCAAGGCGCAAGCACTGATGAGATGTCAACCCAGACGCAATGCGCA 180
Db 308 GTGGGTGCTCAACCAAGGCGCAAGCACTGATGAGATGTCAACCCAGACGCAATGCGCA 367
Cy 181 ACCTGGCCGATGAAGCTGGTGAAGCTGACACACGCGCGGTGTGAGCTAATCGCTATCTC 240
Db 368 ACCTGGCCGATGAAGCTGGTGTGAGCTGACACACGCGCGGTGTGAGCTAATCGCTATCTC 427
Cy 241 GGAATTAATCTGGCGTCAAGCGTCTGTGAGCGAGCTGATTCGCTTAATATGTCGTCGCG 300
Db 428 GGAATTAATCAAGCGCGTCTGTGAGCGAGCTGATTCGCTGAGTAAAGGCGTCGCGCG 487
Cy 301 CAGTCTGTCAGTTCGCGATTAATGCTGATGTCAGACGATACCCGTAATAACAGGCGAA 360
Db 488 CAGTCTGTCAGTTCGCGATTAATGCTGATGTCAGACGATACCCGTAATAACAGGCGAA 547
Cy 361 GCGTTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 420
Db 548 GCGTTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 607
Cy 421 TCCAGTCCCGATCCGTTATTTAATCTCTAATAAACTGGCGTTTCCCACTGATGATACGCG 480
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Db 608 TCCAGTCCCGATCCGTTATTTAATCTCTAATAAACTGGCGTTTCCCACTGATGATACGCG 667
Cy 481 AACGTACTGACGCGATCTCTGAGAGGCGAGAGGGTCAATTTGCTAATCCGGGCAAT 540
Db 668 AACGTACTGACGCGATCTCTGAGAGGCGAGAGGGTCAATTTGCTAATCCGGGCAAT 727
Cy 541 TATCAAGCGCGTTCGCGAAGTGAAGCGGTGCTTAATTTTCGCAATCAACTTGTGC 600
Db 728 CGGCAAGCGCGTTCGCGAAGTGAAGCGGTGCTTAATTTTCGCAATCAACTTGTGC 787
Cy 601 CTTAACGTGAGAAACAGAGAGAAAGCTGTTCAATTAACGAGCAATTAACATCGGAATC 660
Db 788 CTTAACGTGAGAAACAGAGAGAAAGCTGTTCAATTAACGAGCAATTAACATCGGAATC 847
Cy 661 AAGGTAGCGCGCACTGTGCTCATTTAACCGGTGCGTGAACCTTCGATCAATGCTGACG 720
Db 848 AAGGTAGCGCGCACTGTGCTCATTTAACCGGTGCGTGAACCTTCGATCAATGCTGACG 907
Cy 721 GAGATTTTCTCTGCAACAGCAAGGGAATGCGGAGCGCGGGTGGGAAAGATCAAC 780
Db 908 GAGATTTTCTCTGCAACAGCAAGGGAATGCGGAGCGCGGGTGGGAAAGATCAAC 967
Cy 781 GATTCAACAGTGAACACCTTGCTAAGTTGCTAATACGCGCAATTTGATTTGCTACAA 840
Db 968 GATTCAACAGTGAACACCTTGCTAAGTTGCTAATACGCGCAATTTGATTTGCTACAA 1027
Cy 841 CGCAGCGCAGAGTTGCGCGCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 900
Db 1028 CGCAGCGCAGAGTTGCGCGCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1087
Cy 901 TTGAGCGCCCATCCACCGCAAAAACAGCGGTATGCTGATTAACCACTTCAAGTGTG 960
Db 1088 TTGAGCGCCCATCCACCGCAAAAACAGCGGTATGCTGATTAACCACTTCAAGTGTG 1147
Cy 961 TTTATGCGCGACAGATTAATCTGCGAAATCTGCGCGCGCGCACTGAGTCACTGCG 1020
Db 1148 TTTATGCGCGACAGATTAATCTGCGAAATCTGCGCGCGCGCACTGAGTCACTGCG 1207
Cy 1021 ACGCTTCCCGGTCAAGCGGATTAACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1080
Db 1208 ACGCTTCCCGGTCAAGCGGATTAACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1267
Cy 1081 CGTGGCTTAAGGATTAACAGCGAGTGAATCAGTTTGTGCTGCTTCAACCTTTACAG 1140
Db 1268 CGTGGCTTAAGGATTAACAGCGAGTGAATCAGTTTGTGCTGCTTCAACCTTTACAG 1327
Cy 1141 CAGATGCGGATTAACCGCGGTGCTAATTAATAGCGCGCGCGCGAGGTAATCTGACC 1200
Db 1328 CAGATGCGGATTAACCGCGGTGCTAATTAATAGCGCGCGCGCGAGGTAATCTGACC 1387
Cy 1201 CTGGCAGATGTGAAGAGGAAATGCGAGGCGATGTGTTCTGTGCGAGATTTCGCA 1260
Db 1388 CTGGCAGATGTGAAGAGGAAATGCGAGGCGATGTGTTCTGTGCGAGATTTCGCA 1447
Cy 1261 ATCGTGAATGAAGCAAGCATACCGCGGTGCGAGTTTGAAT 1300
Db 1448 ATCGTGAATGAAGCAAGCATACCGCGGTGCGAGTTTGAAT 1487

RESULT 10
US-09-866-379-5
Sequence 5, Application US/09866379
Patent No. US20020136754A1
GENERAL INFORMATION:
APPLICANT: DIVERSA CORPORATION
APPLICANT: SHORT, Jay
APPLICANT: KRETZ, Keith
APPLICANT: GRAY, Kevin
APPLICANT: BARTON, Nelson
APPLICANT: GARRETT, James
APPLICANT: O'DONOGHUE, Eileen
TITLE OF INVENTION: RECOMBINANT BACTERIAL PHYTASES AND USES THEREOF
FILE REFERENCE: DIVER1370-7
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Tue May 4 07:05:31 2004

us-09-866-379d-9.rmp

Page 10

CURRENT APPLICATION NUMBER: US/09/866,379  
CURRENT FILING DATE: 2001-05-24  
PRIOR APPLICATION NUMBER: US 09/580,515  
PRIOR FILING DATE: 2000-05-25  
PRIOR APPLICATION NUMBER: US 09/318,528  
PRIOR FILING DATE: 1999-05-25  
PRIOR APPLICATION NUMBER: US 09/291,931  
PRIOR FILING DATE: 1999-04-13  
PRIOR APPLICATION NUMBER: US 09/259,214  
PRIOR FILING DATE: 1999-03-01  
PRIOR APPLICATION NUMBER: US 08/910,798  
PRIOR FILING DATE: 1997-08-13  
NUMBER OF SEQ ID NOS: 10  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 5  
LENGTH: 1901  
TYPE: DNA  
ORGANISM: Escherichia coli  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (1)..(1901)  
OTHER INFORMATION: n is any nucleotide  
US-09-866-379-5

Query Match 96.5%; Score 1262.2; DB 9; Length 1901;  
Best Local Similarity 98.2%; Pred. No. 0;  
Matches 1276; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

QY 1 ATGAAAGGATCTTAATCCATTTTATCTCTTGTATCCGTTAACCCGCAATTCGA 60  
DB 188 ATGAAAGGATCTTAATCCATTTTATCTCTTGTATCCGTTAACCCGCAATTCGA 247  
QY 61 TTGCGTCAGAGTGGCGGAGCTGAAGCTGAAAGTGTGATGTGTCAGTCGATGGT 120  
DB 248 TTGCGTCAGAGTGGCGGAGCTGAAGTGTGATGTGTCAGTCGATGGT 307  
QY 121 GTGCGTGTCCAAACCAAGGCCACGCACTGATGACGATGTCAACCCGCAAGTGGCA 180  
DB 308 GTGCGTGTCCAAACCAAGGCCACGCACTGATGACGATGTCAACCCGCAAGTGGCA 367  
QY 181 ACCTGCGCGGTAAATCTGAGTGAAGTGAACCGCGCGGTGTGATGATGCTTATCTC 240  
DB 368 ACCTGCGCGGTAAATCTGAGTGAAGTGAACCGCGCGGTGTGATGATGCTTATCTC 427  
QY 241 GGACATTAATCTGCGCTGACGCTGTGATGCGGACGATGCTGCTTAATGTGCTGCCG 300  
DB 428 GGACATTAATCTGCGCTGACGCTGTGATGCGGACGATGCTGCTTAATGTGCTGCCG 487  
QY 301 CAGTCTGTGATGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGAT 360  
DB 488 CAGTCTGTGATGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGAT 547  
QY 361 GCTTCGCGCGCGGCTGACCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCT 420  
DB 548 GCTTCGCGCGCGGCTGACCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCT 607  
QY 421 TCCAGTCCGATCCGTTATTTATCTCTTAATAAATGCGCTTTGCGCACTGGATAGCG 480  
DB 608 TCCAGTCCGATCCGTTATTTATCTCTTAATAAATGCGCTTTGCGCACTGGATAGCG 667  
QY 481 AACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 540  
DB 668 AACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 727  
QY 541 TATCAAAAGCGCTTTGCGCACTGGAACGCGGTCTTAATTTTCCGCAATCAACTGTGCG 600  
DB 728 CGGCAAAAGCGCTTTGCGCACTGGAACGCGGTCTTAATTTTCCGCAATCAACTGTGCG 787  
QY 601 CTTAAAGCGGAAACAGGACGAAAGTGTTCATTAAGCAGGACATTAACATCGGAATC 660  
DB 788 CTTAAAGCGGAAACAGGACGAAAGTGTTCATTAAGCAGGACATTAACATCGGAATC 847  
QY 661 AAGGTGAGCGCCGACTGTGTCTCATTAACGAGTGCCTGTAAGCTTCGATCAATGCTGACG 720

DB 848 AAGGTGAGCGCCGACATGTCTCATTAACGAGTGCCTGTAAGCTTCGATCAATGCTGACG 907  
QY 721 GAGATATTTCTCTCTCAACAAGCAGGGAATGCCAGCGCGGAGTGGGAAGATCAAC 780  
DB 908 GAGATATTTCTCTCTCAACAAGCAGGGAATGCCAGCGCGGAGTGGGAAGATCAAC 967  
QY 781 GATTCAACACAGTGAACAACCTTGTCTTAAGTTTGCATTAACCGCAATTTGATTTGCTACAA 840  
DB 968 GATTCAACACAGTGAACAACCTTGTCTTAAGTTTGCATTAACCGCAATTTGATTTGCTACAA 1027  
QY 841 CGCAGCGCAGAGTGTGCCGCGAGCGCGCAACCCGTTATTAATTTGATCAAGCAGCG 900  
DB 1028 CGCAGCGCAGAGTGTGCCGCGAGCGCGCAACCCGTTATTAATTTGATCAAGCAGCG 1087  
QY 901 TTGACGCGCCATCCACCGCAAAAACAGGCGTATGATGATCAATTAACCACTTCAGTCTG 960  
DB 1088 TTGACGCGCCATCCACCGCAAAAACAGGCGTATGATGATCAATTAACCACTTCAGTCTG 1147  
QY 961 TTATGCGCGGACAGATTAATCTGCAATTAATCTGCGCGGCGCACTGAGTCAACTG 1020  
DB 1148 TTATGCGCGGACAGATTAATCTGCAATTAATCTGCGCGGCGCACTGAGTCAACTG 1207  
QY 1021 ACGCTTCCCGGTCAACCGGATTAACAAGCGCGCGGATGATGATGATGATGATGATGATGAT 1080  
DB 1208 ACGCTTCCCGGTCAACCGGATTAACAAGCGCGCGGATGATGATGATGATGATGATGATGAT 1267  
QY 1081 CGTGGCTTAAGGATTAACAAGCGGATTAACAAGCGGATGATGATGATGATGATGATGATGAT 1140  
DB 1268 CGTGGCTTAAGGATTAACAAGCGGATTAACAAGCGGATGATGATGATGATGATGATGATGAT 1327  
QY 1141 CAGATGCTGATTAACAAGCGGCTGATTAATTAACAAGCGGCTGATTAATTAACAAGCGGCTGAT 1200  
DB 1328 CAGATGCTGATTAACAAGCGGCTGATTAATTAACAAGCGGCTGATTAATTAACAAGCGGCTGAT 1387  
QY 1201 CTGGCAGATGATTAACAAGCGGATTAACAAGCGGCTGATTAATTAACAAGCGGCTGAT 1260  
DB 1388 CTGGCAGATGATTAACAAGCGGATTAACAAGCGGCTGATTAATTAACAAGCGGCTGAT 1447  
QY 1261 ATGCTGATTAACAAGCGGCTGATTAATTAACAAGCGGCTGATTAATTAACAAGCGGCTGAT 1300  
DB 1448 ATGCTGATTAACAAGCGGCTGATTAATTAACAAGCGGCTGATTAATTAACAAGCGGCTGAT 1487  
RESULT 11  
US-09-866-379-9  
Sequence 9, Application US/09866379  
Patent No. US20020136754A1  
GENERAL INFORMATION:  
APPLICANT: DIVERSA CORPORATION  
APPLICANT: SHORT, Jay  
APPLICANT: KREITZ, Keith  
APPLICANT: GRAY, Kevin  
APPLICANT: BARTON, Nelson  
APPLICANT: GARRETT, James  
TITLE OF INVENTION: RECOMBINANT BACTERIAL PHRYASES AND USES THEREOF  
FILE REFERENCE: DIVER1370-7  
CURRENT APPLICATION NUMBER: US/09/866,379  
CURRENT FILING DATE: 2001-05-24  
PRIOR APPLICATION NUMBER: US 09/580,515  
PRIOR FILING DATE: 2000-05-25  
PRIOR APPLICATION NUMBER: US 09/318,528  
PRIOR FILING DATE: 1999-05-25  
PRIOR APPLICATION NUMBER: US 09/291,931  
PRIOR FILING DATE: 1999-04-13  
PRIOR APPLICATION NUMBER: US 09/259,214  
PRIOR FILING DATE: 1999-03-01  
PRIOR APPLICATION NUMBER: US 08/910,798  
PRIOR FILING DATE: 1997-08-13  
NUMBER OF SEQ ID NOS: 10  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 9

```

? LENGTH: 1901
? TYPE: DNA
? ORGANISM: Escherichia coli
? FEATURES:
? NAME/KEY: misc_feature
? LOCATION: (1)..(1901)
? OTHER INFORMATION: n is any nucleotide
US-09-866-379-9

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Query Match	96.5%	Score 1262.2	DB 9	Length 1901
Best Local Similarity	98.2%	Pred. No. 0		
Matches 1276; Conservative	0	Mismatches 24	Indels 0	Gaps 0

Oy	1	TTGAAGGAGATCTTAATCCCATTTTATCTCTTGATTCGGTAAACCCGCAATCTGCA	60
Db	188	ATGAAGGAGATCTTAATCCCATTTTATCTCTTGATTCGGTAAACCCGCAATCTGCA	247
Oy	61	TTCCGTCAGAGTAGACCCGAGCTGAAGCTGGAAAAGTGGTGATTTGTCAGTCGATGCT	120
Db	248	TTCCGTCAGAGTAGACCCGAGCTGAAGCTGGAAAAGTGGTGATTTGTCAGTCGATGCT	307
Oy	121	GTGCGTGTCCAAACCAAGGCCACCGCAACTGATGAGGATGTCACCCGACAGCGCATGCCA	180
Db	308	GTGCGTGTCCAAACCAAGGCCACCGCAACTGATGAGGATGTCACCCGACAGCGCATGCCA	367
Oy	181	ACCTGGCCGGTAAAACTGGGTGAGCTGACACCCGCGCGTGGTGAGCTTAATCGCTAATCTC	240
Db	368	ACCTGGCCGGTAAAACTGGGTGAGCTGACACCGGAGGTGGTGAGCTTAATCGCTAATCTC	427
Oy	241	GGACATTACTGGCGTCAGCGCTGTGTAGCCGACGGAATGTGCTGCTTAATGTGCTGCGC	300
Db	428	GGACATTACCAACGCGACGCGCTGTGTAGCCGACGGAATGTGCTGCTGCGGAAAAAGGGCTGCGCG	487
Oy	301	CAGTGTGTCAGGTGCGGATTTATGCTGATGTGACACAGCGCTACCCGTAATAACAGGGGAA	360
Db	488	CAGTGTGTCAGGTGCGGATTTATGCTGATGTGACACAGCGCTACCCGTAATAACAGGGGAA	547
Oy	361	GCTTTGCGCGCGGGCTGGCACTTGACTGTGCATTAACCGTACAATCCAGGCAAGATACG	420
Db	548	GCTTTGCGCGCGGGCTGGCACTTGACTGTGCATTAACCGTACAATCCAGGCAAGATACG	607
Oy	421	TTCAGTCCCGATCCGTTATTTAATCCCTCTAATAAACTGGCGTTTGCCAATGGATTAACGCG	480
Db	608	TTCAGTCCCGATCCGTTATTTAATCCCTCTAATAAACTGGCGTTTGCCAATGGATTAACGCG	667
Oy	481	AACTGACTGACGCGGATCTCGAGAGGGGACAGAGGGTCAATTGCTGACTTTACCGGGCAT	540
Db	668	AACTGACTGACGCGGATCTCGAGAGGGGACAGAGGGTCAATTGCTGACTTTACCGGGCAT	727
Oy	541	TATCAAAAGGCGGTTTTCGGAAGTGGAAAGGGGTGCTTAATTTTCGCGCATCAAACTGTGC	600
Db	728	CGGCAAAAGGCGGTTTTCGGAAGTGGAAAGGGGTGCTTAATTTTCGCGCATCAAACTGTGC	787
Oy	601	CTTAAGCTGAGAAAACAGAGCGAAAGCTGTTCAATTAAACGACGGCATTAACATCGAAATCTC	660
Db	788	CTTAAGCTGAGAAAACAGAGCGAAAGCTGTTCAATTAAACGACGGCATTAACATCGAAATCTC	847
Oy	661	AAGGAGAGCGCGCATGTGTCTCATTTAACCGGTGGGTAAGCTGCAATCATGTGTAACG	720
Db	848	AAGGAGAGCGCGCGCATGTGTCTCATTTAACCGGTGGGTAAGCTGCAATCATGTGTAACG	907
Oy	721	GAGATATTTCTCTCGAAACAGACCAAGGAAATGCCGAGCCGGGGTGGGAAAGATCAAC	780
Db	908	GAGATATTTCTCTCGAAACAGACCAAGGAAATGCCGAGCCGGGGTGGGAAAGATCAAC	967
Oy	781	GAATTCACACCAATGGAAACCTTGCTAAGTTGCAATTAACGCGCAATTTGATTGCTACAA	840
Db	968	GAATTCACACCAATGGAAACCTTGCTAAGTTGCAATTAACGCGCAATTTGATTGCTACAA	1027
Oy	841	CGCAGCCCAAGAGTTGCCCGACGCCGCGCAACCCGTTATTAGATTGATCAAGACAGC	900
Db	1028	CGCAGCCCAAGAGTTGCCCGACGCCGCGCAACCCGTTATTAGATTGATCAAGACAGC	1087

QY	901	TTACAGCCCATCATCCGCAAAAACAGCGCTATGCTGACATTAACCATTCAGTCG	960
Db	1088	TTACAGCCCATCATCCGCAAAAACAGCGCTATGCTGACATTAACCATTCAGTCG	1147
QY	961	TTTATCGCGGACACGATACTAATCTGGCAATCTCGGCGGCGCATCTGAGCTCACTGG	1020
Db	1148	TTTATCGCGGACACGATACTAATCTGGCAATCTCGGCGGCGCATCTGAGCTCACTGG	1207
QY	1021	ACGCTTCCCGGTCAAGCCGATTAACAGCGCGCCACAGTGGTGAACCTGGGTTGAACGCTGG	1080
Db	1208	ACGCTTCCCGGTCAAGCCGATTAACAGCGCGCCACAGTGGTGAACCTGGGTTGAACGCTGG	1267
QY	1081	CGTCGCGTAAAGCATACAGCCAGTGGATTCAGGTTTCGCTGCTTCACAGCTTTACAG	1140
Db	1268	CGTCGCGTAAAGCATACAGCCAGTGGATTCAGGTTTCGCTGCTTCACAGCTTTACAG	1327
QY	1141	CAGATCGGTATATAAACGCGCTGTCTAATTAATACGCGCCCGGAGAGGTGAACCTGACC	1200
Db	1328	CAGATCGGTATATAAACGCGCTGTCTAATTAATACGCGCCCGGAGAGGTGAACCTGACC	1387
QY	1201	CTGGCAGGATGTGAAGAGCGAAATATCGCCAGAGGCAATGTTGCTTGTTGGAGGTTTACGCA	1266
Db	1388	CTGGCAGGATGTGAAGAGCGAAATATCGCCAGAGGCAATGTTGCTTGTTGGAGGTTTACGCA	1447
QY	1261	ATCGTGAATGAAGACGACATACCGGCGCTGCAGTTTGAGAT	1300
Db	1448	ATCGTGAATGAAGACGACATACCGGCGCTGCAGTTTGAGAT	1487

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RESULT 12
US-10-266-041-9
: Sequence 9, Application US/10266041
: Publication NO. US20030072844A1
: GENERAL INFORMATION:
: APPLICANT: lei, xigen
: TITLE OF INVENTION: ENZYMES WITH IMPROVED PHYTASE ACTIVITY
: FILE REFERENCE: 19603/2791
: CURRENT APPLICATION NUMBER: US/10/266,041
: CURRENT FILING DATE: 2002-10-07
: PRIOR APPLICATION NUMBER: US/09/540,149
: PRIOR FILING DATE: 2000-03-31
: PRIOR APPLICATION NUMBER: 60/127,032
: PRIOR FILING DATE: 1999-03-31
: NUMBER OF SEQ ID NOS: 9
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 9
: LENGTH: 1489
: TYPE: DNA
: ORGANISM: Escherichia coli
US-10-266-041-9

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Query Match	93.9%	Score 1228;	DB 15.	Length 1489;
Best Local Similarity	96.5%	Pred. No. 0;		
Matches 1255;	Conservative	0;	Mismatches 45;	Indels 0;
				Gaps 0

QY	1	TTGAAGGACCTTAATCCATTTTAACTCTTCGATTCGCTGAACCCGGAACTGGA	60
Db	182	ATGAAGGACTTTAAATCCATTTTAACTCTTTGAATTCGCTGAACCCGGAACTGGA	241
QY	61	TTCCGCTCAGAGTGAACCCGGAGCTGAAGCTGGAAATGTGTGATGTCAATGCTAATGGT	120
Db	242	TTCCGCTCAGAGTGAACCCGGAGCTGAAGCTGGAAATGTGTGATGTCAATGCTAATGGT	301
QY	121	GTGCGTGTCCAAACCGAAGGCCACGCAATGACGATGTCAACCCGACGATGGCCA	180
Db	302	GTGCGTGTCCAAACCGAAGGCCACGCAATGACGATGTCAACCCGACGATGGCCA	361
QY	181	ACCTGGCCGGTAAACTGGGTGAGGTGACACCGCGCGGTGTGTGAAGCTAATGCGCTAATGC	240
Db	362	ACCTGGCCGGTAAACTGGGTGAGGTGACACCGCGGTGTGTGAAGCTAATGCGCTAATGC	421
QY	241	GGACATTACTGGCGTCAACGCTGTGGTAGCCGACGAGATTGCTGCTPAATGTGGCTGGCCCG	300



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Db 422 GGAATTACCAAGCCAGCGTCTGTGCGCCAGCGAATGCTGCGGAAAAAGGCGTCCCG 481
QY 301 CAGCTTGTGTCAGGTGCGGATTAATGCTGATGTCAGAGCGTACCCGTAAACAGGCGAA 360
Db 482 CAGCTGTGTGAGGTGCGGATTAATGCTGATGTCAGAGCGTACCCGTAAACAGGCGAA 541
QY 361 GCGTGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 420
Db 542 GCGTGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 601
QY 421 TCCAGTCCCGATCCGTTATTTAATCTCTAATAAACTGCGCTTTCGCACTGATTAACGC 480
Db 602 TCCAGTCCCGATCCGTTATTTAATCTCTAATAAACTGCGCTTTCGCACTGATTAACGC 661
QY 481 AACGTGACGTGACGCGATCTCTGAGAGGCGAGAGGTCATGCTGACTTAACCGGCGAT 540
Db 662 AACGTGACGTGACGCGATCTCTGAGAGGCGAGAGGTCATGCTGACTTAACCGGCGAT 721
QY 541 TATCAAAACGCGGTTTCGCGAATGGAACGCGGCTTAATTTCCGCAATCAAACTTGTGC 600
Db 722 CCGGAAACGCGGTTTCGCGAATGGAACGCGGCTTAATTTCCGCAATCAAACTTGTGC 781
QY 601 CTCTAAACGTGGAACAGAGAGAAAGCTGTTCAATTAACGAGGATTAACCATCGGAATC 660
Db 782 CTCTAAACGTGGAACAGAGAGAAAGCTGTTCAATTAACGAGGATTAACCATCGGAATC 841
QY 661 AAGGTGACGCGCGACTGTGTCTCATTAACGCGGTGCGTAAGCTCGCATCAATGCTGACG 720
Db 842 AAGGTGACGCGCGACTGTGTCTCATTAACGCGGTGCGTAAGCTCGCATCAATGCTGACG 901
QY 721 GAGATATTTCTCTGCAACAAAGCAAGGAAATGCCGAGCGCGGCTGGGAAAGATCAAC 780
Db 902 GAAATATTTCTCTGCAACAAAGCAAGGAAATGCCGAGCGCGGCTGGGAAAGATCAAC 961
QY 781 GATTCAACACAGTGAACACCTTGTGTAAGTTGATTAACGCGCAATTTGATTTGCTCAAA 840
Db 962 GATTCAACACAGTGAACACCTTGTGTAAGTTGATTAACGCGCAATTTGATTTGCTCAAA 1021
QY 841 CGCAGCGCAAGGTTCCCGCGACCGCGCGCACCCCGTATTATTAATTTGATTAACAGCG 900
Db 1022 CGCAGCGCAAGGTTCCCGCGACCGCGCGCACCCCGTATTATTAATTTGATTAACAGCG 1081
QY 901 TTGACGCGCGCATCAACCGCAAAACAGGCGTATGCTGATTAACCATTTCACTGCTG 960
Db 1082 TTGACGCGCGCATCAACCGCAAAACAGGCGTATGCTGATTAACCATTTCACTGCTG 1141
QY 961 TTTATCGCGGACACGATTAATCTGCAAAATCTGCGCGCGCATGAGACTCACTG 1020
Db 1142 TTTATCGCGGACACGATTAATCTGCAAAATCTGCGCGCGCATGAGACTCACTG 1201
QY 1021 ACGCTTCCCGTCAACCGGATTAACAGCGCGCGCATGAGACTGTTGAAAGCGCTG 1080
Db 1202 ACGCTTCCCGTCAACCGGATTAACAGCGCGCGCATGAGACTGTTGAAAGCGCTG 1261
QY 1081 CGTCCGCTAAGGATTAACAGCGCGATGATTCAGGTTTGTGCTGCTTCCAGACTTTAAG 1140
Db 1262 CGTCCGCTAAGGATTAACAGCGCGATGATTCAGGTTTGTGCTGCTTCCAGACTTTAAG 1321
QY 1141 CAGATGCGGTGATTAACCGCGCTGCTCATTTAATAGCGCGCGCGGAGAGGTAACTGACC 1200
Db 1322 CAGATGCGGTGATTAACCGCGCTGCTCATTTAATAGCGCGCGCGGAGAGGTAACTGACC 1381
QY 1201 CTGCGAGGATGTAAGAGGAAATGCGAGGCGCATGTTGCTGTTGCGAGTTTACGCA 1260
Db 1382 CTGCGAGGATGTAAGAGGAAATGCGAGGCGCATGTTGCTGTTGCGAGTTTACGCA 1441
QY 1261 ATCGTGAATGAAGCAAGCATACCGCGCTGCACTTTGAGAT 1300
Db 1442 ATCGTGAATGAAGCAAGCATACCGCGCTGCACTTTGAGAT 1481

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RESULT 13  
US-10-284-962-1

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/ Sequence 1, Application US/10284962
/ Publication No. US20030206913A1
/ GENERAL INFORMATION:
/ APPLICANT: Weibel, Douglas M.
/ APPLICANT: Orr, Donald E.
/ APPLICANT: Ruch, Frank E.
/ TITLE OF INVENTION: PHYTASE-CONTAINING ANIMAL FOOD AND METHOD
/ FILE REFERENCE: 834460-71725
/ CURRENT APPLICATION NUMBER: US/10/284,962
/ PRIOR FILING DATE: 2002-10-31
/ PRIOR APPLICATION NUMBER: US 60/335,303
/ NUMBER OF SEQ ID NOS: 14
/ SOFTWARE: Patent in version 3.1
/ SEQ ID NO. 1
/ LENGTH: 1489
/ TYPE: DNA
/ ORGANISM: Escherichia coli
/ FEATURE:
/ NAME/KEY: primer_bind
/ LOCATION: (1)..(22)
/ OTHER INFORMATION:
/ FEATURE:
/ NAME/KEY: primer_bind
/ LOCATION: (1468)..(1489)
/ OTHER INFORMATION:
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (16)..(108)
/ OTHER INFORMATION:
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (182)..(1480)
/ OTHER INFORMATION:
/ US-10-284-962-1

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Query Match 93.9%; Score 1228; DB 16; Length 1489;
Best Local Similarity 96.5%; Pred. No. 0;
Matches 1255; Conservative 0; Mismatches 45; Indels 0; Gaps 0;
QY 1 ATGAAAGCATCTTAATCCCAATTTTATCTCTTCTGATTCCTGTTAACCCCGCAATCTGCA 60
Db 182 ATGAAAGCATCTTAATCCCAATTTTATCTCTTCTGATTCCTGTTAACCCCGCAATCTGCA 241
QY 61 TTGCTCAAGAGTGAAGCGGAGCTGAAGTGAAGTGTGATGATGTCATGCTGATGCT 120
Db 242 TTGCTCAAGAGTGAAGCGGAGCTGAAGTGAAGTGTGATGATGTCATGCTGATGCT 301
QY 121 GTGCGTCTCCAAACCAAGGCGCAAGCACTGATGCAAGATGTCAACCCAGAGCGATGGCA 180
Db 302 GTGCGTCTCCAAACCAAGGCGCAAGCACTGATGCAAGATGTCAACCCAGAGCGATGGCA 361
QY 302 GTGCGTCTCCAAACCAAGGCGCAAGCACTGATGCAAGATGTCAACCCAGAGCGATGGCA 361
Db 181 ACCTGCGCGTAAATCTGCGTGAAGTGAACAGCGCGCGTGTGAGCTAATCGCTATCTC 240
QY 181 ACCTGCGCGTAAATCTGCGTGAAGTGAACAGCGCGCGTGTGAGCTAATCGCTATCTC 240
Db 362 ACCTGCGCGTAAATCTGCGTGAAGTGAACAGCGCGCGTGTGAGCTAATCGCTATCTC 421
QY 241 GGAATTACTGCGGTGAGCGCTGCTGTAAGCGGATGCTGCTGCTAATGTTGCTGCGCG 300
Db 422 GGAATTACTGCGGTGAGCGCTGCTGTAAGCGGATGCTGCTGCTAATGTTGCTGCGCG 481
QY 422 GGAATTACTGCGGTGAGCGCTGCTGTAAGCGGATGCTGCTGCTAATGTTGCTGCGCG 481
Db 301 CAGTCTGTGCAAGTCCGCGATTAATGCTGATGTCAGAGCGTAAACCGGTAAACAGGCGAA 360
QY 301 CAGTCTGTGCAAGTCCGCGATTAATGCTGATGTCAGAGCGTAAACCGGTAAACAGGCGAA 360
Db 482 CAGCTGTGTCAGGTGCGGATTAATGCTGATGTCAGAGCGTAAACCGGTAAACAGGCGAA 541
QY 482 CAGCTGTGTCAGGTGCGGATTAATGCTGATGTCAGAGCGTAAACCGGTAAACAGGCGAA 541
Db 542 GCGTGTGCGCGCGCGGCTGCGCACTGACTGTGCAATACGTAATCCAGGCGAGTACG 601
QY 542 GCGTGTGCGCGCGGCTGCGCACTGACTGTGCAATACGTAATCCAGGCGAGTACG 601
Db 601 GCGTGTGCGCGCGGCTGCGCACTGACTGTGCAATACGTAATCCAGGCGAGTACG 601
QY 601 GCGTGTGCGCGCGGCTGCGCACTGACTGTGCAATACGTAATCCAGGCGAGTACG 601
Db 421 TCCAGTCCCGATCCGTTATTTAATCTCTAATAAACTGCGCTTTCGCACTGATTAACGC 480
QY 421 TCCAGTCCCGATCCGTTATTTAATCTCTAATAAACTGCGCTTTCGCACTGATTAACGC 480
Db 602 TCCAGTCCCGATCCGTTATTTAATCTCTAATAAACTGCGCTTTCGCACTGATTAACGC 661
QY 602 TCCAGTCCCGATCCGTTATTTAATCTCTAATAAACTGCGCTTTCGCACTGATTAACGC 661
Db 481 AACGTGACGTGACGCGATCTCTGAGAGGCGAGAGGTCATGCTGACTTAACCGGCGAT 540

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Db	662	AACGTGACTGACGGATCTCAGCAGGGCAGGAGGGTCAATTGCTGACTTTACCGGCAAT	721
QY	541	TATCAAAACGCGGTTTCGGCAACTGGAACGGGTCTTAAATTTTCGGCAATCAAACTTGTGC	600
Db	722	CGGCAAAACGCGGTTTCGGCAACTGGAACGGGTCTTAAATTTTCGGCAATCAAACTTGTGC	781
QY	601	CTTAAACGTGAGAAACAGACGAAAGCGTTTCATTAACGACGCACTTACCATCGGCACTC	660
Db	782	CTTAAACGTGAGAAACAGACGAAAGCGTTTCATTAACGACGCACTTACCATCGGCACTC	841
QY	661	AAGGTGACCGCCGACTGTCTCATTTAACCGGTGCGTAAAGCTTCGCATCAATGCTGACG	720
Db	842	AAGGTGACCGCCGCAATGTTCATTTAACCGGTGCGTAAAGCTTCGCATCAATGCTGACG	901
QY	721	GAGATTTTTCCTTCACAACAACAAGCGGAGACCGGGGTGGGGAGATTCAC	780
Db	902	GAAATATTTCTCTCCACAACAGCAAGGAAATCCGAGACCGGGGTGGGGAGATTCAC	961
QY	781	GATTCAACACAGTGGAAACCTTGTCTAAGTTTGCATTAACGCGCAATTTGATTTGCTACA	840
Db	962	GATTCAACACAGTGGAAACCTTGTCTAAGTTTGCATTAACGCGCAATTTGATTTGCTACA	1022
QY	841	CGCAACCCAGAGTTGCCCGCAGCCGCCACCCCGTTTATTAAGATTTGATCAAGACGCG	900
Db	1022	CGCAACCCAGAGTTGCCCGCAGCCGCCACCCCGTTTATTAAGATTTGATCAAGACGCG	1081
QY	901	TTGACGCCCCATCCACCGCAAAAACAGGCGTATGTTGTGACATTAACCCACTTCAGTGTG	960
Db	1082	TTGACGCCCCATCCACCGCAAAAACAGGCGTATGTTGTGACATTAACCCACTTCAGTGTG	1141
QY	961	TTTATGCGCGACACGATCTATCTATCTGGCAATCTTGCGCGGCGCACTGAGCTCAACTG	1022
Db	1142	TTTATGCGCGACACGATCTATCTATCTGGCAATCTTGCGCGGCGCACTGAGCTCAACTG	1201
QY	1021	ACGCTTCCCGGTCAGCGCGGATTAACACCGCCAGGTGGTGAATCGTGTGTTAAAGCTG	1080
Db	1202	ACGCTTCCCGGTCAGCGCGGATTAACACCGCCAGGTGGTGAATCGTGTGTTAAAGCTG	1261
QY	1081	CGTCGGCTPAAGCGATPAACGACGATGATTCAGGTTTGCCTGCTTCTTCAGACTTTACAG	1141
Db	1262	CGTCGGCTPAAGCGATPAACGACGATGATTCAGGTTTGCCTGCTTCTTCAGACTTTACAG	1321
QY	1141	CAGATCGCGTGAATAAACCGCGCTGCATTAATAACGCGCGCGGAGAGGTGAACCTGAC	1200
Db	1322	CAGATCGCGTGAATAAACCGCGCTGCATTAATAACGCGCGCGGAGAGGTGAACCTGAC	1381
QY	1201	CTGGCAGATGTGAAGAGCGAATGCGACAGGCAATGTGTCGTGGCAGGTTTAAACGAA	1260
Db	1382	CTGGCAGATGTGAAGAGCGAATGCGACAGGCAATGTGTCGTGGCAGGTTTAAACGAA	1441
QY	1261	ATCGTGAATGAAGACACGCAATCCGGGTGCTCAGTTTGAGT	1300
Db	1442	ATCGTGAATGAAGACCGGCACTACCGGGGTGCTCAGTTTGAGT	1481

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/ RESULT 14
/ US-10-284-962-A
/ Sequence 4, Application US/10284962
/ Publication No. US20030206913A1
/ GENERAL INFORMATION:
/ APPLICANT: Weibel, Douglas M.
/ APPLICANT: Orr, Donald E.
/ APPLICANT: Ruch, Frank E.
/ TITLE OF INVENTION: PHTAS5-CONTAINING ANIMAL FOOD AND METHOD
/ FILE REFERENCE: 834460-7/11725
/ CURRENT APPLICATION NUMBER: US/10/284,962
/ CURRENT FILING DATE: 2002-10-31
/ PRIOR APPLICATION NUMBER: US 60/335,303
/ PRIOR FILING DATE: 2001-10-31
/ NUMBER OF SEQ ID NOS: 14
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 4

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; LENGTH: 1486
; TYPE: DNA
; ORGANISM: Escherichia coli
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (188)..(1483)
; OTHER INFORMATION:
US-10-284-962-4

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Query Match	93.5%	Score 1222.4;	DB 16;	Length 1486;
Best Local Similarity	96.5%;	Pred. No. 0;		
Matches 1250;	Conservative	0;	Mismatches 46;	Indels 0;
				Gaps 0;

QY	1	ATGAAAGCATCTTAAATCCCATTTTATCTCTTCTGTATTCOCTTAACCCGCAATCTGCA	60
Db	188	ATGAAAGCATCTTAAATCCCATTTTATCTCTTCTGTATTCOCTTAACCCGCAATCTGCA	247
QY	61	TTTGCTCAGATGTAGCCGAGCTGAGCTGGAAGATGTGATGTCTAGTCTCATGTGT	120
Db	248	TTTGCTCAGATGTAGCCGAGCTGAGCTGGAAGATGTGATGTCTAGTCTCATGTGT	307
QY	121	GTGCGTGTCTCAACCAAGGCCACGCAACTGATGCAAGATGTCAACCCAGACGCAATGCGCA	180
Db	308	GTGCGTGTCTCAACCAAGGCCACGCAACTGATGCAAGATGTCAACCCAGACGCAATGCGCA	367
QY	181	ACCTGGCCGGTAAAACTGGGTGAGCTGACACCGCGCGGTGTGAGCTATCGCTATCTC	240
Db	368	ACCTGGCCGGTAAAACTGGGTGAGCTGAGCAACCGCGGTGTGAGCTATCTATCTC	427
QY	241	GAACATTACTGGCGTACGCGTCTGTGTAGACCGAGATTTGCTCTAAATGTGCTGCCG	300
Db	428	GAACATTACTGGCGTACGCGTCTGTGTAGACCGAGATTTGCTCTAAATGTGCTGCCG	487
QY	301	CAGCTGTGTACAGTCCGGATTAATGTGTGATGTGACAGAGGTACCCGTAAACAGCGCAA	360
Db	488	CAGCTGTGTACAGTCCGGATTAATGTGTGATGTGACAGAGGTACCCGTAAACAGCGCAA	547
QY	361	GCTTTGCGCGCGGGCTGGCACTGTGTGCAATTAACCGTACATCCAGGCAAGATACG	420
Db	548	GCTTTGCGCGCGGGCTGGCACTGTGTGCAATTAACCGTACATCCAGGCAAGATACG	607
QY	421	TTCAGTCCCGATCCGTTATTTAATCTCTTAAAACTGGCGTTTGTGCCAATGGGAATAACGG	480
Db	608	TTCAGTCCCGATCCGTTATTTAATCTCTTAAAACTGGCGTTTGTGCCAATGGGAATAACGG	667
QY	481	AACGTGACTGACGCGATCTCGAAGAGGCGAGAGGATCAATTGTGACTTTACCGGGCAT	540
Db	668	AACGTGACTGACGCGATCTCGAAGAGGCGAGAGGATCAATTGTGACTTTACCGGGCAT	727
QY	541	TATCAACGCGCGTTTCGGAACGTGAAACGGGTGCTTAAATTTTCGCAATCAAATCTGTGC	600
Db	728	CGGCAAAACGGCGTTTCGGAACGTGAAACGGGTGCTTAAATTTTCGCAATCAAATCTGTAC	787
QY	601	CTTAAAGCTGAGAAACAGGACGAAGAGCTGTCATTAAACGACGCAATTCATCCGCAATC	660
Db	788	CTTAAAGCTGAGAAACAGGACGAAGAGCTGTCATTAAACGACGCAATTCATCCGCAATC	847
QY	661	AAGGTAGCGCGCACTGTGTCTCATTTAACGCGTGTGCTGTAAGCTTGTGCATCATGTGACG	720
Db	848	AAGGTAGCGCGCACTGTGTCTCATTTAACGCGTGTGCTGTAAGCTTGTGCATCATGTGACG	907
QY	721	GAGATATTTCCTCGACCAAGCAACGAGGAATGCGGAGCGGGGTGGGGAAGATCAAC	780
Db	908	GAGATATTTCCTCGACCAAGCAACGAGGAATGCGGAGCGGGGTGGGGAAGATCACT	967
QY	781	GATTCAACACAGTGAACACCTTGTCTAATGTTGCATAACGCGCAATTTGATTTGCTACAA	840
Db	968	GATTCAACACAGTGAACACCTTGTCTAATGTTGCATAACGCGCAATTTTATTACTACAA	1027
QY	841	CGACGCCAGAGGTGGCCCGACGCGGCGCAACCCGCTATTAGATTTGATCAAGCACGCG	900
Db	1028	CGACGCCAGAGGTGGCCCGACGCGGCGCAACCCGCTATTAGATTTGATCAAGCACGCG	1087

QY 901 TTGAGCCCATTCACCGCAAAAACAGCGTATGTGTGACATTACCACTTCACTGTCTG 960  
Db 1088 TTGAGCCCATTCACCGCAAAAACAGCGTATGTGTGACATTACCACTTCACTGTCTG 1147  
QY 961 TTGATGCGCGGACAGCACTAATCTATCTGCGCAAAATCTGCGCGCGACACTGAGCTCACTG 1020  
Db 1148 TTGATGCGCGGACAGCACTAATCTATCTGCGCAAAATCTGCGCGCGACACTGAGCTCACTG 1207  
QY 1021 ACCTTCCTCCGCTACGCGGATPACACGCGCGGAGTGTAACTGTGTTTGAACGCTG 1080  
Db 1208 ACCTTCCTCCGCTACGCGGATPACACGCGCGGAGTGTAACTGTGTTTGAACGCTG 1267  
QY 1081 CGTGGCTAAGCGGATPACAGCACTGATTCAGTTTCTGCTGCTTCCAGCTTTTACAG 1140  
Db 1268 CGTGGCTAAGCGGATPACAGCACTGATTCAGTTTCTGCTGCTTCCAGCTTTTACAG 1327  
QY 1141 CAGATGCGGTAAACAGCGCGCTGTCTATTAATACGCGCGCGAGAGTGAACCTGACC 1200  
Db 1328 CAGATGCGGTAAACAGCGCGCTGTCTATTAATACGCGCGCGAGAGTGAACCTGACC 1387  
QY 1201 CTGGCAGGATGTGAAGAGCGCAATGCGGCACTGTGTCTGTGGAGAGTTTACGCA 1260  
Db 1388 CTGGCAGGATGTGAAGAGCGCAATGCGGCACTGTGTCTGTGGAGAGTTTACGCA 1447  
QY 1261 ATCGTGAATGAAGCAGCATACCGGCGGTGACGTTTG 1296  
Db 1448 ATCGTGAATGAAGCAGCATACCGGCGGTGACGTTTG 1483

## RESULT 15

US-10-334-672-4  
; Sequence 4, Application US/10334672  
; Publication No. US20030157646A1  
; GENERAL INFORMATION:  
; APPLICANT: Lananhan, Mike  
; APPLICANT: Koepf, Edward  
; APPLICANT: Kretz, Keith  
; TITLE OF INVENTION: Microbially-Expressed Thermotolerant Phytase For Animal Feed  
; FILE REFERENCE: SYNG-P01-001  
; CURRENT APPLICATION NUMBER: US/10/334,672  
; PRIOR FILING DATE: 2002-12-30  
; PRIOR APPLICATION NUMBER: 60/344,523  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 4  
; LENGTH: 1281  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: No. US20030157646A19X gene  
US-10-334-672-4

Query Match 52.9%; Score 691.4; DB 15; Length 1281;  
Best Local Similarity 72.4%; Pred. No. 8,1e-233;  
Matches 896; Conservative 0; Mismatches 341; Indels 0; Gaps 0;

QY 64 GCTCAAGTGAAGCGGAGCTGAAGCTGAAAGTGTGGTATTCAGTCTCATGTGTG 123  
Db 28 GCTCAATCTGAACAGCAATTTGAAGTGGAACTGTGTCTCATTTGCTCCAGACAGGTTT 87  
QY 124 CGTGTCCAAACCAAGGCGCAACTGATGCAAGATGTCACCCAGACGATGSCCAAC 183  
Db 88 AGAGTCCAACTAAGCTCACTCACTGATGATGCAAGATGTTACTCCAGATGTGSCCTAC 147  
QY 184 TGGCCGCTAAACCTGGTGAAGCTGACACCGCGCGGTGTGAGCTTAATGCTTACTGGA 243  
Db 148 TGGCCGCTTAAGTGGTGAAGTGAATGATCTCCAGAGGTGTGAATGATGCTTACTTGGGT 207  
QY 244 CATTAAGTGAAGCTGTGTGTGAGCGGAGATTTGCTTAATATGTGCTGCGCCAG 303  
Db 208 CATTAAGTGAAGCTGTGTGTGAGCGGAGATTTGCTTAATATGTGCTGCGCCAG 267

QY 304 TCTGTCAAGTGTGCGATTAATTTGCTGATGTGACAGAGGTAACCCGTAATAACAGCGGAG 363  
Db 268 TCTGTCAAGTGTGCGATTAATTTGCTGATGTGATGATTAATAAGATTAATAAGCTGGAAG 327  
QY 364 TTGCGCGCGGCTGGGCACTGATGTGCAATACCGTATACCCAGAGATACGTTCC 423  
Db 328 TTGCGCGCGGCTGGGCACTGATGTGCAATACCGTATACCCAGAGATACGTTCC 387  
QY 424 AGTCCGATTCGCTTAATTAATCTTAAATACTGCGCTTGGCCACTGATTAAGCCGAC 483  
Db 388 TCTCCAGATTCATTTGTTCAACCACTTGAAGATGATGTGTCTGCTCAATTTGATTAAGCTTAC 447  
QY 484 GTGATGACGCGATCTGAGAGGAGGACAGAGGTCATTAATGCTGACTTACCGGCAATTA 543  
Db 448 GTTACTGATGCGATTTTGGAAAGAGCTGTGTGTCTATGCTGATCTTCACTGATCACTAC 507  
QY 544 CAACGCGGCTTTCGGAACGGAACGAGTGTCTTAATTTTCCGCAATCAACTTGTGCTT 603  
Db 508 CAACGCGCTTTCAGAGAAATGGAAGATGTTGAACCTTCCCAATCTTAATCTGTGTTG 567  
QY 604 AATCGTGAAGAAACAGAGAGAAAGCTGTCTTAACGAGGATTAACATCGGAATCAAG 663  
Db 568 AATCGTGAAGAAACAGAGAGAAATCTTGTCTTGAATCAAGCTTGCATCTGAATGAG 627  
QY 664 GTGAGCGCGACTGTGTCTCAATTAACCGGTGCGGTAAAGCTCGATCAATGCTGACGAG 723  
Db 628 GTCTGCTGATGTGTGTCTCTTCTGATGCTGTGCTGTCTTCTGCTTCAATGTTGAGAA 687  
QY 724 ATATTTCTCTGCAACAGCAACAGGAAATGCGGAGCGCGGCTGGGAGAGATCAAGAT 783  
Db 688 ATCTTCTTGTGCAACAGCTCAAGTATGCGAGAACAGGTTGGGAGATCACTGAT 747  
QY 784 TCACACAGTGAACACCTGTGTAATGCTTAACGCGCAATTTGATGCTCAACAGC 843  
Db 748 TCTCAACATGGAACACCTGTGTGCTTGTGCAACAGCTCAATGATTTGCTGAGAGA 807  
QY 844 AGCGGAGGTTGCGCGGAGCGCGCCACCCCGTTATTGATTTGATTAACAGCGTTG 903  
Db 808 ACTCAAGAGTGTGCTGATTAACAGAGCTCACTGATTTGATGATTAACAGCGTTG 867  
QY 904 AGCGGCAATCCACCGCAAAAACAGCGCTATGATGATTAATCACTTCACTGCTGTT 963  
Db 868 ACTCAACCCACACAGAGAGAGCTTAAGGTGTGATCTTGTGCACTTGTGCTGCTG 927  
QY 964 ATGCGCGACAGATTAATCTGCAAAATCTGCGCGCGCACTGAGCTCACTGACG 1023  
Db 928 ATGCGCGCTCAAGATTAATCTTGTGCTAACTTGTGCTGCTGCAATTAAGCTGAC 987  
QY 1024 CTTCGCGCTCAGCGGATTAACAGCGCGCAGGTGTGAATGTTGATTAAGCTGCGCT 1083  
Db 988 TTGCGAGCTCAACAGATTAACCTCACAGGTGTGAATTTGCTTGAAGATGCGGT 1047  
QY 1084 CGGCTAAGCGATTAACAGCAAGTGAATTCAGGTTTGTCTTCCAGACTTTACAGAG 1143  
Db 1108 ATGAGAGCAAGATCTCATTTGCTTGAACCTCACAGGTGAATGAATGATGCTG 1167  
QY 1204 GAGAGATGAAGAGCAAAATGCGAGGCAATGTGTGTTGAGGTTTACGCAATC 1263  
Db 1168 GCTGTGTGAGAGAAAGAGCTCAAGGTATGTGTCTTGTGCTGAGTTCACTCAATC 1227  
QY 1264 GTGAATGAAGCAGATTAACCGCGCTGCAATTTGAAT 1300  
Db 1228 GTCAAGAGAGCAAGATTCAGCTGTCTTGAAT 1264

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Job time : 535.107 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: May 1, 2004, 21:37:37 ; Search time 104.347 Seconds  
(without alignments)  
6956.396 Million cell updates/sec

Title: US-09-866-379D-9  
Perfect score: 1308  
Sequence: 1 atgaagcgcatactatcc.....gcagttcgagatctcacta 1308

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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2: /cgn2\_6/ptodata/2/ina/5B.COMB.seq:\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1265	96.7	1323	3	US-09-259-214-1
2	1265	96.7	1323	3	US-09-318-528-1
3	1265	96.7	1323	3	US-09-291-931-1
4	1228	93.9	1489	4	US-09-540-149A-9
5	1153	88.1	1272	2	US-08-910-798-1
6	66.2	5.1	1266	4	US-09-489-039A-341
7	39.8	3.0	505	4	US-09-621-976-15639
8	36.6	2.8	2868	4	US-09-710-794-4
9	34.4	2.6	4403765	3	US-09-103-840A-2
10	34.4	2.6	4411529	3	US-08-103-840A-1
11	34.2	2.6	4403765	3	US-09-103-840A-2
12	34.2	2.6	4411529	3	US-09-103-840A-1
13	34	2.6	998	2	US-07-885-089B-5
14	33.8	2.6	399	4	US-09-621-976-8976
15	33	2.5	2511	2	US-08-680-326-116
16	33	2.5	35100	2	US-08-770-379-17
17	33	2.5	35100	3	US-08-757-668A-17
18	33	2.5	35100	3	US-09-230-371A-17
19	32.6	2.5	3147	1	US-08-441-430-3
20	32.6	2.5	4485	4	US-09-023-655-1286
21	32.6	2.5	4488	1	US-08-441-430-1
22	32.2	2.5	2430	4	US-09-489-039A-1732
23	32.2	2.5	3076	4	US-09-710-794-1
24	32	2.4	1533	4	US-09-489-039A-4607
25	31.8	2.4	474	4	US-09-621-976-18033
26	31.8	2.4	480	4	US-09-252-991A-15917
27	31.8	2.4	762	4	US-09-252-991A-15888

C 28	31.8	2.4	885	4	US-09-252-991A-15774	Sequence 15774, A
C 29	31.8	2.4	1068	4	US-09-252-991A-15804	Sequence 15804, A
C 30	31.6	2.4	505	4	US-09-621-976-15639	Sequence 15639, A
C 31	31.2	2.4	825	4	US-09-489-039A-172	Sequence 172, App
C 32	31.2	2.4	1034	4	US-09-072-596-312	Sequence 312, App
C 33	31.2	2.4	1034	4	US-09-072-596-317	Sequence 317, App
C 34	31	2.4	498	4	US-09-252-991A-7289	Sequence 7289, Ap
C 35	31	2.4	966	4	US-09-252-991A-7468	Sequence 7468, Ap
C 36	31	2.4	1329	4	US-09-489-039A-3268	Sequence 3268, Ap
C 37	31	2.4	1563	4	US-09-252-991A-7226	Sequence 7226, Ap
C 38	31	2.4	1734	4	US-08-857-636-58	Sequence 58, App1
C 39	31	2.4	3753	5	PCT-US95-02251-2	Sequence 2, App1
C 40	31	2.4	3759	3	US-08-479-722B-3	Sequence 3, App1
C 41	31	2.4	4314	1	US-08-199-780-2	Sequence 2, App1
C 42	31	2.4	4314	2	US-08-316-650-2	Sequence 2, App1
C 43	30.8	2.4	1491	4	US-09-540-236-920	Sequence 920, App
C 44	30.8	2.4	94750	4	US-09-596-002-38	Sequence 38, App1
C 45	30.6	2.3	1086	4	US-09-489-039A-3528	Sequence 3528, Ap

## ALIGNMENTS

RESULT 1  
US-09-259-214-1  
Sequence 1, Application US/09259214A  
Patent No. 6110719  
GENERAL INFORMATION:  
APPLICANT: Kretz, Keith  
TITLE OF INVENTION: NOVEL PHYTASE  
FILE REFERENCE: DIVER1370-1  
CURRENT APPLICATION NUMBER: US/09/259,214A  
CURRENT FILING DATE: 1999-03-01  
EARLIER APPLICATION NUMBER: 08/910,798  
EARLIER FILING DATE: 1997-08-13  
NUMBER OF SEQ ID NOS: 4  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 1  
LENGTH: 1323  
TYPE: DNA  
ORGANISM: Escherichia coli  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (1)...(1320)  
NAME/KEY: misc.feature  
LOCATION: (1)...(1323)  
OTHER INFORMATION: n = A,T,C or G  
US-09-259-214-1

Query Match 96.7%; Score 1265; DB 3; Length 1323;  
Best Local Similarity 98.0%; Pred. No. 0;  
Matches 1280; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

QY	1	ATGAAGCAGTCTTAATCCATTTTATCTCTGATTCGGTAACCCGCAATCGA	60
DB	1	ATGAAGCAGTCTTAATCCATTTTATCTCTGATTCGGTAACCCGCAATCGA	60
QY	61	TTGCTCTAGAGTGAAGCCGAGTGAAGCTGGAAGTGTGATTTCTAGTCTATG	120
DB	61	TTGCTCTAGAGTGAAGCCGAGTGAAGCTGGAAGTGTGATTTCTAGTCTATG	120
QY	121	GTGGGTGCTCCAGCAGGCGACGAACTGATGACAGATGTACACCCAGACGATG	180
DB	121	GTGGGTGCTCCAGCAGGCGACGAACTGATGACAGATGTACACCCAGACGATG	180
QY	181	ACCTGCGCGTAAACTGAGTGAAGTGAACCGCGGTGTGAGCTAATCGCTATCT	240
DB	181	ACCTGCGCGTAAACTGAGTGAAGTGAACCGCGGTGTGAGCTAATCGCTATCT	240
QY	241	GGACATTAACGAGGCTGAGGCTGAGGCGAGATGCTGCTAAATGAGGCTGCG	300
DB	241	GGACATTAACGAGGCTGAGGCTGAGGCGAGATGCTGCTAAATGAGGCTGCG	300

301 CAGCTGTGAGGTCGAGTATTTGATGTGACGAGGTCACCCGTAACAGAGCGAA 360  
301 CAGCTGTGAGGTCGAGTATTTGATGTGACGAGGTCACCCGTAACAGAGCGAA 360  
361 GCCTTCGCGCGGCTGCGACCTGACTGTGCAATTAACGTAATCCAGAGATAGC 420  
361 GCCTTCGCGCGGCTGCGACCTGACTGTGCAATTAACGTAATCCAGAGATAGC 420  
421 TCCAGTCCGATCCGCTATTTATCTCTTAAATCTGCGCTTCCGCACTGATTAACGC 480  
421 TCCAGTCCGATCCGCTATTTATCTCTTAAATCTGCGCTTCCGCACTGATTAACGC 480  
481 AACGTGACTGACGCGATCTCTGAGAGAGGCGAGAGGTCATTTGCTGACTTTACCGGCA 540  
481 AACGTGACTGACGCGATCTCTGAGAGAGGCGAGAGGTCATTTGCTGACTTTACCGGCA 540  
541 TATTAACGCGGCTTTCGCGAACTGAAACGGGCTTTAATTTTCGCAATCAACTTGTGC 600  
541 CCGCAACGCGGCTTTCGCGAACTGAAACGGGCTTTAATTTTCGCAATCAACTTGTGC 600  
601 CTTAAACGTGAGAAACAGAGAGAGGTCCTTATTAACGAGCATTAACATCGAACTC 660  
601 CTTAAACGTGAGAAACAGAGAGAGGTCCTTATTAACGAGCATTAACATCGAACTC 660  
661 AAGGTGAGCGCGACTGTGTCTCTTAACGCGGTGCGTAAAGCTTCGATCAATGCTGACG 720  
661 AAGGTGAGCGCGACTGTGTCTCTTAACGCGGTGCGTAAAGCTTCGATCAATGCTGACG 720  
721 GAGATATTTCTCTCTGCAACAGAGAGGTCGAGAGCGGCGTGGAGAGATCAC 780  
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781 GATTCAACAGAGTGAACACCTTCTTAAGTTGCAATTAACGCGCAATTTGATTTGCTCA 840  
781 GATTCAACAGAGTGAACACCTTCTTAAGTTGCAATTAACGCGCAATTTGATTTGCTCA 840  
841 CGCAGCGCAGAGTGTGCGCGCGAGCGCGACCCGCTATTAAGTTGATTAACAGAGCG 900  
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1261 ATCGTGAATGAAGACGATACCGGCGTGCAGTTGAGATCTATC 1306  
1261 ATCGTGAATGAAGACGATACCGGCGTGCAGTTGAGATCTATC 1306

RESULT 2  
US-09-318-528-1  
; Sequence 1, Application US/09318528  
; Patent No.: 6183740

GENERAL INFORMATION:  
APPLICANT: Krenz, Keith  
TITLE OF INVENTION: NOVEL PHRASE  
FILE REFERENCE: 09/010/029003  
CURRENT APPLICATION NUMBER: US/09/318,528  
CURRENT FILING DATE: 1999-05-25  
EARLIER APPLICATION NUMBER: 09/291,931  
EARLIER FILING DATE: 1999-04-13  
EARLIER APPLICATION NUMBER: 08/910,798  
EARLIER FILING DATE: 1997-08-13  
EARLIER APPLICATION NUMBER: 09/259,214  
EARLIER FILING DATE: 1999-03-01  
NUMBER OF SEQ ID NOS: 4  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 1  
LENGTH: 1323  
TYPE: DNA  
ORGANISM: Escherichia coli  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (1)...(1320)  
NAME/KEY: misc feature  
LOCATION: (1)...(1323)  
OTHER INFORMATION: n = A,T,C or G  
US-09-318-528-1  
Query Match 96.7%; Score 1265; DB 3; Length 1323;  
Best Local Similarity 98.0%; Pred. No. 0;  
Matches 1280; Conservative 0; Mismatches 26; Indels 0; Gaps 0;  
1 ATGAAGGAGATCTTATCCATTTTATCTCTGATTCGCTTAACCCGCAATTCGCA 60  
1 ATGAAGGAGATCTTATCCATTTTATCTCTGATTCGCTTAACCCGCAATTCGCA 60  
61 TTGCTCAGAGTGAACCGAGAGTGAAGTGTGATGATTCAGTGTGATGAT 120  
61 TTGCTCAGAGTGAACCGAGAGTGAAGTGTGATGATTCAGTGTGATGAT 120  
121 GTGCTGTCTCCACCAAGCCGACGATGATGATGATGATGATGATGATGAT 180  
121 GTGCTGTCTCCACCAAGCCGACGATGATGATGATGATGATGATGATGAT 180  
181 ACCCTGCGGTAAACTGAGTGAAGTGAACGAGCGGTGAGTGAATGCTATCTC 240  
181 ACCCTGCGGTAAACTGAGTGAAGTGAACGAGCGGTGAGTGAATGCTATCTC 240  
241 GACATTAATGAGGTCAGGCTGATGATGATGATGATGATGATGATGATGAT 300  
241 GACATTAATGAGGTCAGGCTGATGATGATGATGATGATGATGATGATGAT 300  
301 GAGTGTGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 360  
301 GAGTGTGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 360  
361 GCCTTCGCGCGGCTGCGACCTGACTGTGCAATTAACGTAATCCAGAGATAGC 420  
361 GCCTTCGCGCGGCTGCGACCTGACTGTGCAATTAACGTAATCCAGAGATAGC 420  
421 TCCAGTCCGATCCGCTATTTATCTCTTAAATCTGCGCTTCCGCACTGATTAACGC 480  
421 TCCAGTCCGATCCGCTATTTATCTCTTAAATCTGCGCTTCCGCACTGATTAACGC 480  
481 AACGTGACTGACGCGATCTCTGAGAGAGGCGAGAGGTCATTTGCTGACTTTACCGGCA 540  
481 AACGTGACTGACGCGATCTCTGAGAGAGGCGAGAGGTCATTTGCTGACTTTACCGGCA 540  
541 TATTAACGCGGCTTTCGCGAACTGAAACGGGCTTTAATTTTCGCAATCAACTTGTGC 600  
541 TATTAACGCGGCTTTCGCGAACTGAAACGGGCTTTAATTTTCGCAATCAACTTGTGC 600  
601 CTTAAACGTGAGAAACAGAGAGAGGTCCTTATTAACGAGCATTAACATCGAACTC 660  
601 CTTAAACGTGAGAAACAGAGAGAGGTCCTTATTAACGAGCATTAACATCGAACTC 660

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QY 661 AAGGTAGGCGCGCATCTGTCTCTATTAACCGGTGCGGTAAAGCTCGCATCATCTGACG 720
DB 661 AAGGTAGGCGCGCATCTGTCTCTATTAACCGGTGCGGTAAAGCTCGCATCATCTGACG 720
QY 721 GAGATATTTCTCTCTGCAACAGACAGAGAAATGCGGAGCCGGGTGGGAAAGATCAAC 780
DB 721 GAGATATTTCTCTCTGCAACAGACAGAGAAATGCGGAGCCGGGTGGGAAAGATCAAC 780
QY 781 GATTCAACACAGTGAACAACCTTGTGAAGTTTGATTAACCGCAATTGATTTGCTACAA 840
DB 781 GATTCAACACAGTGAACAACCTTGTGAAGTTTGATTAACCGCAATTGATTTGCTACAA 840
QY 841 CGCAGCGCAGAGGTTCGCGCGACGCGCGCAACCCGTTATGATTGATTAACAAGACGCG 900
DB 841 CGCAGCGCAGAGGTTCGCGCGACGCGCGCAACCCGTTATGATTGATTAACAAGACGCG 900
QY 901 TTGACGCGCCCATCCACCGCAAAAACAGCGGTATGATGAACATTACCACTTCAAGTCTG 960
DB 901 TTGACGCGCCCATCCACCGCAAAAACAGCGGTATGATGAACATTACCACTTCAAGTCTG 960
QY 961 TTTATGCGCGGACACGATCTAATCTGCGAAATCTGCGCGGCGCACTGAGAGTCAACTG 1020
DB 961 TTTATGCGCGGACACGATCTAATCTGCGAAATCTGCGCGGCGCACTGAGAGTCAACTG 1020
QY 1021 ACGCTTCCCGGTGACGCGGATTAACAGCGCGCAAGTGTGAACCTGATGTTTGAACGCTG 1080
DB 1021 ACGCTTCCCGGTGACGCGGATTAACAGCGCGCAAGTGTGAACCTGATGTTTGAACGCTG 1080
QY 1081 CGTGGCGTAAAGCATTAACAGCGGTGATTCAGGTTTCGCTGCTTTCCAGACTTTACG 1140
DB 1081 CGTGGCGTAAAGCATTAACAGCGGTGATTCAGGTTTCGCTGCTTTCCAGACTTTACG 1140
QY 1141 CAGATGCGATTAATAAGCGCGTGTCTAATTAATACCGCGCGCGGAGAGTGAACCTGAC 1200
DB 1141 CAGATGCGATTAATAAGCGCGTGTCTAATTAATACCGCGCGCGGAGAGTGAACCTGAC 1200
QY 1201 CTGGCAGAGATGAAGAAGCAAAATGCGCAGGCGCATGTTGCGAGGTTTACGCA 1260
DB 1201 CTGGCAGAGATGAAGAAGCAAAATGCGCAGGCGCATGTTGCGAGGTTTACGCA 1260
QY 1261 ATGTGAATGAAGCAGCATTAACGCGGTGACGTTTGATCTCATC 1306
DB 1261 ATGTGAATGAAGCAGCATTAACGCGGTGACGTTTGATCTCATC 1306

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## RESULT 3

US-09-291-931-1

Sequence 1, Application US/09291931A

Patent No. 6190897

GENERAL INFORMATION:

APPLICANT: Kretz, Keith

TITLE OF INVENTION: NOVEL PHYTASE

FILE REFERENCE: 09010/029003

CURRENT APPLICATION NUMBER: US/09/291,931A

EARLIER FILING DATE: 1999-04-13

EARLIER APPLICATION NUMBER: 08/910,798

EARLIER FILING DATE: 1997-06-13

EARLIER APPLICATION NUMBER: 09/259,214

NUMBER OF SEQ ID NOS: 4

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 1

LENGTH: 1323

TYPE: DNA

ORGANISM: Escherichia coli

FEATURE:

NAME/KEY: CDS

LOCATION: (1) ... (1320)

NAME/KEY: misc feature

LOCATION: (1) ... (1323)

OTHER INFORMATION: n = A,T,C or G

US-09-291-931-1

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Query Match 96.7%; Score 1265; DB 3; Length 1323;
Best Local Similarity 98.0%; Pred. No. 0;
Matches 1280; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

QY 1 ATGAAGCGATCTTAATCCATTTTATCTCTCTGATTCGTTTACCCCGCAATCTGCA 60
DB 1 ATGAAGCGATCTTAATCCATTTTATCTCTCTGATTCGTTTACCCCGCAATCTGCA 60
QY 61 TTGCGTCAAGTGAAGCGGAGCTGAAGCTGAAGAGTGTGATGCTGATGCTGATGCT 120
DB 61 TTGCGTCAAGTGAAGCGGAGCTGAAGCTGAAGAGTGTGATGCTGATGCTGATGCT 120
QY 121 GTGCGTGTCCCAACCAAGGCGCAACGCACTGATGAGATGCAACCCGACGATGCGCA 180
DB 121 GTGCGTGTCCCAACCAAGGCGCAACGCACTGATGAGATGCAACCCGACGATGCGCA 180
QY 181 ACTGCGCGGTAAACTGAGTGAAGCTGACACCGCGCGGTGTGAGCTTAATCGCTATCT 240
DB 181 ACTGCGCGGTAAACTGAGTGAAGCTGACACCGCGCGGTGTGAGCTTAATCGCTATCT 240
QY 241 GGAATTAATCTGAGCGTCAAGCGTCTGATAGCGGACGGAATTGCTGCTTAATGTGCTG 300
DB 241 GGAATTAATCTGAGCGTCAAGCGTCTGATAGCGGACGGAATTGCTGCTTAATGTGCTG 300
QY 301 CAGTGTGTCAGTGTGCGGATTAATCTGATGTGCAAGAGGTAAACCGGTAAACAGGCGAA 360
DB 301 CAGTGTGTCAGTGTGCGGATTAATCTGATGTGCAAGAGGTAAACCGGTAAACAGGCGAA 360
QY 361 GCGTTGCGCGCGGCGTGGGACCTGACTGTCGCAATTAACCGTACCAAGCGAGATACG 420
DB 361 GCGTTGCGCGCGGCGTGGGACCTGACTGTCGCAATTAACCGTACCAAGCGAGATACG 420
QY 421 TCCAGTCCCGATCCGTTATTTTAACTCTCTAATAAATCGGCTTTGCCAATGGAATACG 480
DB 421 TCCAGTCCCGATCCGTTATTTTAACTCTCTAATAAATCGGCTTTGCCAATGGAATACG 480
QY 481 AACGTAATGAAGGATTCCTGAGAGGCGGAGAGGATCAATGCTGCTTAACCGGAGAT 540
DB 481 AACGTAATGAAGGATTCCTGAGAGGCGGAGAGGATCAATGCTGCTTAACCGGAGAT 540
QY 541 TATCAAGCGGCTTTCGGAATCGGAACGCGGTCTTAATTTTCGCAATCAAACTGTGC 600
DB 541 TATCAAGCGGCTTTCGGAATCGGAACGCGGTCTTAATTTTCGCAATCAAACTGTGC 600
QY 601 CTTAAAGCTGAAGAACAGAGAGGATCTTCAATTAACGAGGATTAACCAATCGGAATCT 660
DB 601 CTTAAAGCTGAAGAACAGAGAGGATCTTCAATTAACGAGGATTAACCAATCGGAATCT 660
QY 661 AAGGTAGGCGCGCATCTGTCTCTAATTAACCGGTGCGGTAAAGCTCGATCAATCTGAC 720
DB 661 AAGGTAGGCGCGCATCTGTCTCTAATTAACCGGTGCGGTAAAGCTCGATCAATCTGAC 720
QY 721 GAGATATTTCTCTCTGCAACAGACAGGAAATGCGGAGCCGGGTGGGAAAGATCAAC 780
DB 721 GAGATATTTCTCTCTGCAACAGACAGGAAATGCGGAGCCGGGTGGGAAAGATCAAC 780
QY 781 GATTCAACACAGTGAACAACCTGCTAAGTTTGCAACGCGCAATTGATTTGCTACAA 840
DB 781 GATTCAACACAGTGAACAACCTGCTAAGTTTGCAACGCGCAATTGATTTGCTACAA 840
QY 841 CGCAGCGCAGAGGTTCGCGCGACGCGCGCAACCCGTTATGATTGATTAACAAGACGCG 900
DB 841 CGCAGCGCAGAGGTTCGCGCGACGCGCGCAACCCGTTATGATTGATTAACAAGACGCG 900
QY 901 TTGACGCGCCCATCCACCGCAAAAACAGCGGTATGATGAACATTACCACTTCAAGTCTG 960
DB 901 TTGACGCGCCCATCCACCGCAAAAACAGCGGTATGATGAACATTACCACTTCAAGTCTG 960
QY 961 TTTATGCGCGGACACGATCTAATCTGCGAAATCTGCGCGGCGCACTGAGAGTCAACTG 1020
DB 961 TTTATGCGCGGACACGATCTAATCTGCGAAATCTGCGCGGCGCACTGAGAGTCAACTG 1020

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QY 1021 AGCTTCCCGCTCAGCCGAGTAACACGCCCGCAGGTGTAACTGTGTGTAAGAGCTGG 1080
DB 1021 AGCTTCCCGCTCAGCCGAGTAACACGCCCGCAGGTGTGTAAGAGCTGTGTAAGAGCTGG 1080
QY 1081 CGTGGCTAAGCGATTAACAGCCAGTGTGATTCAGGTTTGGTGTCTTCCAGACTTTACAG 1140
DB 1081 CGTGGCTAAGCGATTAACAGCCAGTGTGATTCAGGTTTGGTGTCTTCCAGACTTTACAG 1140
QY 1141 CAGATGCGGTATTAACAGCCGCTGTCTATTAATATACCGCCGAGAGGTGAAGCTGACC 1200
DB 1141 CAGATGCGGTATTAACAGCCGCTGTCTATTAATATACCGCCGAGAGGTGAAGCTGACC 1200
QY 1201 CTGCGCAGATGTGAAGAGCGAAATGCGCAGGGCATGTGTGTCAGAGTTTACGCA 1260
DB 1201 CTGCGCAGATGTGAAGAGCGAAATGCGCAGGGCATGTGTGTCAGAGTTTACGCA 1260
QY 1261 ATGCTGAATGAACACGCGATACCGGGGTGATGATTCATC 1306
DB 1261 ATGCTGAATGAACACGCGATACCGGGGTGATGATTCATC 1306

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## RESULT 4

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US-09-540-149A-9
; Sequence 9, Application US/09540149A
; Patent No. 6511699
; GENERAL INFORMATION:
; APPLICANT: Le1, Xinggen
; TITLE OF INVENTION: ENZYMES WITH IMPROVED PHYTASE ACTIVITY
; FILE REFERENCE: 19603/2791
; CURRENT APPLICATION NUMBER: US/09/540,149A
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 60/127,032
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 1489
; TYPE: DNA
; ORGANISM: Escherichia coli
US-09-540-149A-9

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Query Match 93.9%; Score 1228; DB 4; Length 1489;
Best Local Similarity 96.5%; Pred. No. 0;
Matches 1255; Conservative 0; Mismatches 45; Indels 0; Gaps 0;

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QY 1 ATGAAAGCGATCTTAATCCCATTTTATCTCTGATTCGGTTAACCCGCAATCTGCA 60
DB 182 ATGAAAGCGATCTTAATCCCATTTTATCTCTGATTCGGTTAACCCGCAATCTGCA 241
QY 61 TTGCTCAGAGTGAAGCCGAGCTGAAGCTGGAAGTGTGTGATTTGTCATGTATGT 120
DB 242 TTGCTCAGAGTGAAGCCGAGCTGAAGCTGGAAGTGTGTGATTTGTCATGTATGT 301
QY 121 GTGCTGCTCAACCAAGGCCAAGCACTGATGAGATGTCACCCAGAGCATGAGCCA 180
DB 302 GTGCTGCTCAACCAAGGCCAAGCACTGATGAGATGTCACCCAGAGCATGAGCCA 361
QY 362 ACCTGCGCGTAAACTGGGTGAGCTGACACCGCGCGGTGATGATTCATTCCTATCTC 240
DB 421 ACCTGCGCGTAAACTGGGTGAGCTGACACCGCGCGGTGATGATTCATTCCTATCTC 481
QY 422 GGAATTAACCAACGCGACGCTGTGTGCGCAGAGATTTGCGGAGAAAGGCTGCGCG 300
DB 481 GGAATTAACCAACGCGACGCTGTGTGCGCAGAGATTTGCGGAGAAAGGCTGCGCG 441
QY 482 CAGCTGCTCAGAGTGAAGCTGATTTGCTGATGTCAGACGAGCTTACCCGTAAGAGG 360
DB 541 CAGCTGCTCAGAGTGAAGCTGATTTGCTGATGTCAGACGAGCTTACCCGTAAGAGG 420
QY 542 GCTTTCGCGCGCGGCTGACCTGATGTCATTAACCGTAACCCAGAGCGAGATGACG 601

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QY 421 TCCAGTCCCGATCCGTATTATTAATCTCTTAATAACTGCGCTTTGCCACTGATTAAGCG 480
DB 602 TCCAGTCCCGATCCGTATTATTAATCTCTTAATAACTGCGCTTTGCCACTGATTAAGCG 661
QY 481 AAGGTGACTGACGCGATCTCTGAGAGGGGAGAGGGTCAATTGCTGACTTACCGGACAT 540
DB 662 AAGGTGACTGACGCGATCTCTGAGAGGGGAGAGGGTCAATTGCTGACTTACCGGACAT 721
QY 541 TATCAACGCGGCTTCCGCAACTGGAACGAGTGTCTTAATTTTCCGATCAAACTGTGTC 600
DB 722 CCGCAACGCGGCTTCCGCAACTGGAACGAGTGTCTTAATTTTCCGATCAAACTGTGTC 781
QY 601 CTTAAACGTGAGAAACAGAGCGAAAGCTGTCTTAATGAGAGCACTTACATGAGAACTC 660
DB 782 CTTAAACGTGAGAAACAGAGCGAAAGCTGTCTTAATGAGAGCACTTACATGAGAACTC 841
QY 661 AAGGTGACGCGCATCTGTCTCTTAATACCGGTGAGTAAAGCTGATCAATGTGACG 720
DB 842 AAGGTGACGCGCATCTGTCTCTTAATACCGGTGAGTAAAGCTGATCAATGTGACG 901
QY 721 GAGATATTTCTCTGCAACAGCAAGGAAATGCGGAGCCGAGGTGGGAAAGATCAC 780
DB 902 GAAATATTTCTCTGCAACAGCAAGGAAATGCGGAGCCGAGGTGGGAAAGATCAC 961
QY 781 GATTCAACAGAGTGAACACCTTCTTAAGTTTGATTAACCGCAATTTGATTTGCTACAA 840
DB 962 GATTCAACAGAGTGAACACCTTCTTAAGTTTGATTAACCGCAATTTGATTTGCTACAA 1021
QY 841 CGCAGCGCAGAGTGTGCGCGCAGCGCGCCAGCCCGCTTATTAAGTTTGAATCAACAGCG 900
DB 1022 CGCAGCGCAGAGTGTGCGCGCAGCGCGCCAGCCCGCTTATTAAGTTTGAATCAACAGCG 1081
QY 901 TTGACGCGCCATCAACAGCAAGGAGTGAATGATGATTAACCACTTCACTGCTG 960
DB 1082 TTGACGCGCCATCAACAGCAAGGAGTGAATGATGATTAACCACTTCACTGCTG 1141
QY 961 TTTATGCGCGCAACAGATTAATCTGCAAAATCTGCGCGCGCACTGAGCTTAATCTG 1020
DB 1142 TTTATGCGCGCAACAGATTAATCTGCAAAATCTGCGCGCGCACTGAGCTTAATCTG 1201
QY 1021 AGCTTCCCGCTCAGCCGAGTAACACGCCCGCAGGTGTAACTGTGTGTAAGAGCTGG 1080
DB 1202 AGCTTCCCGCTCAGCCGAGTAACACGCCCGCAGGTGTAACTGTGTGTAAGAGCTGG 1261
QY 1081 CGTGGCTAAGCGATTAACAGCCAGTGTGATTCAGGTTTGGTGTCTTCCAGACTTTACAG 1140
DB 1262 CGTGGCTAAGCGATTAACAGCCAGTGTGATTCAGGTTTGGTGTCTTCCAGACTTTACAG 1321
QY 1141 CAGATGCGGTATTAACAGCCGCTGTCTATTAATATACCGCCGAGAGGTGAAGCTGACC 1200
DB 1322 CAGATGCGGTATTAACAGCCGCTGTCTATTAATATACCGCCGAGAGGTGAAGCTGACC 1381
QY 1201 CTGCGCAGATGTGAAGAGCGAAATGCGCAGGGCATGTGTGTCAGAGTTTACGCA 1260
DB 1382 CTGCGCAGATGTGAAGAGCGAAATGCGCAGGGCATGTGTGTCAGAGTTTACGCA 1441
QY 1261 ATGCTGAATGAACACGCGATACCGGGGTGATGATTCATC 1300
DB 1442 ATGCTGAATGAACACGCGATACCGGGGTGATGATTCATC 1481

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## RESULT 5

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US-08-910-798-1
; Sequence 1, Application US/08910798
; Patent No. 5876997
; GENERAL INFORMATION:
; APPLICANT: KREIZ
; TITLE OF INVENTION: NOVEL PHYTASE
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla

```

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STATE: California
COUNTRY: US
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/910,798
FILING DATE: August 13,1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: HAILE, PH.D., LISA A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 09010/029001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
TELEFAX: 619/678-5099
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1272 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
IMMEDIATE SOURCE:
CLONE: PHYLASE
FEATURE:
NAME/KEY:
LOCATION:
US-08-910-798-1

Query Match      88.1%; Score 1153; DB 2; Length 1272;
Best Local Similarity 94.1%; Pred. No. 0;
Matches 1229; Conservative 0; Mismatches 26; Indels 51; Gaps 1;

QY 1 ATGAAGCATCTTAATCCATTTTATCTCTTGTGATTCGTTAACCCCGCAATCTGCA 60
DB 1 ATGAAGCATCTTAATCCATTTTATCTCTTGTGATTCGTTAACCCCGCAATCTGCA 60
QY 61 TTGCGTCAGAGTGAAGCCGAGCTGAAGCTGAAAGTGTGTGATTTGTAGTGTGATGCT 120
DB 61 TTGCGTCAGAGTGAAGCCGAGCTGAAGCTGAAAGTGTGTGATTTGTAGTGTGATGCT 120
QY 121 GTGCGGTCTCCAAACCAAGGCCACGCACTGATGACAGATGTCAACCCGAGAGCATGGCA 180
DB 121 GTGCGGTCTCCAAACCAAGGCCACGCACTGATGACAGATGTCAACCCGAGAGCATGGCA 180
QY 181 ACCTGCGCGGTAAACCTGGGTGAGCTGACACCGCGGTGTGAGTAAATGCGCTATCTC 240
DB 181 ACCTGCGCGGTAAACCTGGGTGAGCTGACACCGCGGTGTGAGTAAATGCGCTATCTC 240
QY 241 GGACATTAATCTGGCGTCAAGGCTGTGAGCCAGCGGATTTGCTGCTAAATGTGGCTGCCG 300
DB 241 GGACATTAATCTGGCGTCAAGGCTGTGAGCCAGCGGATTTGCTGCTGCTGCTGCCG 300
QY 301 CAGTGTGTCAGGTGCGGATTAATGCTGATGTGACGAGCCGTACCCGTAAACAGGCGAA 360
DB 301 CAGTGTGTCAGGTGCGGATTAATGCTGATGTGACGAGCCGTACCCGTAAACAGGCGAA 360
QY 361 GCGTTCGCGCGCGGGCTGGCACTGCTGTAATACCGTACATACCCAGGCGAGATGCG 420
DB 361 GCGTTCGCGCGCGGGCTGGCACTGCTGTAATACCGTACATACCCAGGCGAGATGCG 420
QY 421 TCCAGTCCCGATCCGTTATTTATCTCTTAATCTGAGGCTTGGCACTGATGATACCGG 480
DB 421 TCCAGTCCCGATCCGTTATTTATCTCTTAATCTGAGGCTTGGCACTGATGATACCGG 480
QY 481 AACGTGATGAGCGGATCTCGAGAGGCGAGAGGCTCAATTGCTGACTTTTACCGGGCAT 540
DB 481 AACGTGATGAGCGGATCTCGAGAGGCGAGAGGCTCAATTGCTGACTTTTACCGGGCAT 540
QY 540 AACGTGATGAGCGGATCTCGAGAGGCGAGAGGCTCAATTGCTGACTTTTACCGGGCAT 540
DB 540 AACGTGATGAGCGGATCTCGAGAGGCGAGAGGCTCAATTGCTGACTTTTACCGGGCAT 540

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QY 541 TATCAACCGCGCTTTCGCACTGGAACGGGTGCTTAATTTCCGCAATCAACTTTCG 600
DB 490 CGGCAACCGCGCTTTCGCACTGGAACGGGTGCTTAATTTCCGCAATCAACTTTCG 549
QY 601 CTTAAACGTGAGAAACAGAGAGAAAGCTGTTCATTAACGAGGATTCACATCGGAACTC 660
DB 550 CTTAAACGTGAGAAACAGAGAGAAAGCTGTTCATTAACGAGGATTCACATCGGAACTC 609
QY 661 AAGGTAGGCGCGGACTGTGCTCTATTAAACGGGTGCGTAAAGCTGCAATGCTGACG 720
DB 610 AAGGTAGGCGCGGACTGTGCTCTATTAAACGGGTGCGTAAAGCTGCAATGCTGACG 669
QY 721 GAATATTTCTCTGTAACAGGAAACAGGAAATCCCGGAGCCGGGTGGGGAAGATACCC 780
DB 670 GAATATTTCTCTGTAACAGGAAACAGGAAATCCCGGAGCCGGGTGGGGAAGATACCC 729
QY 781 GATTCAACCAAGTGAACAACCTTGATTTGATTAACGCGCAATTTGATTTGCTACAA 840
DB 730 GATTCAACCAAGTGAACAACCTTGATTTGATTAACGCGCAATTTGATTTGCTACAA 789
QY 841 CGCAGCGCAGAGGTTCGCGCAGCGCGCCGCAACCCGTTATTGATTTGATTAAGACAGG 900
DB 790 CGCAGCGCAGAGGTTCGCGCAGCGCGCCGCAACCCGTTATTGATTTGATTAAGACAGG 849
QY 901 TTGACGCCCATTCACCGCAAAAACAGGCGTANGTGTGACATTACCCACTTCAAGTCTG 960
DB 850 TTGACGCCCATTCACCGCAAAAACAGGCGTANGTGTGACATTACCCACTTCAAGTCTG 909
QY 961 TTTATGCGCGGACACGATTAATCTTGGCAATCTTCCGCGCGGACCTGAGCTCAACTG 1020
DB 910 TTTATGCGCGGACACGATTAATCTTGGCAATCTTCCGCGCGGACCTGAGCTCAACTG 969
QY 1021 AAGCTTCCCGGTGAGCGCGGATTAACGCGCGGAGGAGTGAATGCTGTTGAACGCTG 1080
DB 970 AAGCTTCCCGGTGAGCGCGGATTAACGCGCGGAGGAGTGAATGCTGTTGAACGCTG 1029
QY 1081 CGTGGGCTAAGCATTAACGCGGATGATGATGCTGCTGCTTCCGCTTCCGACTTTACG 1140
DB 1030 CGTGGGCTAAGCATTAACGCGGATGATGATGCTGCTGCTTCCGCTTCCGACTTTACG 1089
QY 1141 CAGATGCGGTAAACCGCGCTGTGATTAATTAACCGCGCGCGGAGGAGTGAACCTGACC 1200
DB 1090 CAGATGCGGTAAACCGCGCTGTGATTAATTAACCGCGCGCGGAGGAGTGAACCTGACC 1149
QY 1201 CTGCGAGATGTGAAGAGCAATGCGCAGGAGCATGTGCTGTGCAAGTTTTCGCA 1260
DB 1150 CTGCGAGATGTGAAGAGCAATGCGCAGGAGCATGTGCTGTGCAAGTTTTCGCA 1209
QY 1261 ATGCTGATTAAGACGCGATACCGGCGTGCAGTTTAAGATTCATC 1306
DB 1210 ATGCTGATTAAGACGCGATACCGGCGTGCAGTTTAAGATTCATC 1255

RESULT 6
US-09-489-039A-341
Sequence 341, Application US/09489039A
Patent No. 6610836
GENERAL INFORMATION:
APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709,2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
PRIORITY FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 341
LENGTH: 1266
TYPE: DNA
ORGANISM: Klebsiella pneumoniae
US-09-489-039A-341

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[illegible]

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Yy 311GGCGGATTAATTCGCGATGATGCGACGACCGTAACCCGTAACAAAGGCGAAGCCCTTCGCCGCC 372
Db 129 MEFRRRRKRYTMMKTYMMMSWMCYRKGAANTYMSAPARITATASACACMSGRMMKMSNMW 70
Yy 373 GGGCTGCGACCTGACGTGTGCAATTAACCGTACATATCCAGGACAGATACGTCCAGTCCCAT 432
Db 69 MCGMSRYRVCWMSGKWCYSCCGYCCSACRFICYMTIRKMSWYSRSKSRMCCRYSMSMSAY 10
Yy 433 CCGTATTT 441
Db 9 RYSSRRTXT 1

RESULT 8
US-09-710-794-4/C
; Sequence 4, Application US/09710794
; Patent No. 6573069
; GENERAL INFORMATION:
; APPLICANT: Holloway, James L.
; APPLICANT: Gao, Zeren
; APPLICANT: Whitmore, Theodore E.
; TITLE OF INVENTION: NOVEL CRIB PROTEIN ZMSL
; FILE REFERENCE: 99-76
; CURRENT APPLICATION NUMBER: US/09/710.794
; CURRENT FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: US 60/164,685
; PRIOR FILING DATE: 1999-11-10
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FaetsHQ for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 2868
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (173)...(1219)
US-09-710-794-4

Query Match 2.8%; Score 36.6; DB 4; Length 2868;
Best Local Similarity 52.3%; Pred.No.0.13;
Matches 81; Conservative 0; Mismatches 74; Indels 0; Gaps 0

Yy 128 CTCGCAACCAAGCCGACGCAATGATGAGATGTCACCCGACGCGATGCGCAACTGCGC 187
Db 353 CTGCCTCCTCGGCTCTGTAGTAGGAAGAGGTGTCCCAAGAGGTCCCGACGCCGCC 294
Yy 188 CGGTAAACTGCGGTGANGCTGACACCGCGCGGTGTGAGCTAATCGCTTAATCTGGACAT 247
Db 293 CCACATGATGATGTGTGTGGGGAAGTACCCACGCGGAGCATGATCACTCGGCTGTAGGT 234
Yy 248 ACTGGCGTCAGCGCTGTGTAAGCCGACGAGATTGCTG 282
Db 233 CCGCACGTGAGCGGCGCTTCGAGTTCACAGACTG 199

RESULT 9
US-09-103-840A-2
; Sequence 2, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: PRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103.840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1.
; SEQ ID NO 2
; LENGTH: 4403765

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TYPE: DNA  
ORGANISM: Mycobacterium tuberculosis  
FEATURE:  
OTHER INFORMATION: CDC 1551  
OTHER INFORMATION: "n" bases at various positions throughout the sequence  
OTHER INFORMATION: represent a, t, c or g  
US-09-103-840A-2

Query Match 2.6%; Score 34.4; DB 3; Length 4403765;  
Best Local Similarity 52.9%; Pred. No. 50;  
Matches 74; Conservative 0; Mismatches 66; Indels 0; Gaps 0;

QY 262 CTGGAGCCGACGAGATTGCTGCTTAATGCTGCTCCCGCAGTCTGTGACAGTGCAGATT 321  
DB 3709961 CAGGTGCGCCCCGCACTGCTGAAATCCCTGCTGCGGAGCTGACTGCAGCCAAATC 3710020  
QY 322 ATTGCTGATGTCGACGAGCGTAAACCGCGAAGCCTTGCCCGCGGCTGACA 381  
DB 3710021 GTCCGCGAAGCCGCGGAGTGAACCGGTTCAAAAGCGAAGCCGCTTGCCCATGCC 3710080  
QY 382 CCTGACTGTGAATACCGT 401  
DB 3710081 GCAGTGCTCCATCCCGGT 3710100

RESULT 10  
US-09-103-840A-1

Sequence 1, Application US/09103840A  
Patent No. 6294328  
GENERAL INFORMATION:  
APPLICANT: FLEISCHMAN, Robert D.  
APPLICANT: WHITE, Owen R.  
APPLICANT: FRASER, Claire M.  
APPLICANT: VENTER, John C.  
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM  
FILE REFERENCE: 24366-2007.00  
CURRENT APPLICATION NUMBER: US/09/103,840A  
CURRENT FILING DATE: 1998-06-24  
NUMBER OF SEQ ID NOS: 2  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 1  
LENGTH: 4411529  
TYPE: DNA  
ORGANISM: Mycobacterium tuberculosis  
OTHER INFORMATION: H37Rv  
US-09-103-840A-1

Query Match 2.6%; Score 34.4; DB 3; Length 4411529;  
Best Local Similarity 52.9%; Pred. No. 50;  
Matches 74; Conservative 0; Mismatches 66; Indels 0; Gaps 0;

QY 262 CTGGAGCCGACGAGATTGCTGCTTAATGCTGCTCCCGCAGTCTGTGACAGTGCAGATT 321  
DB 3712396 CAGGTGCGCCCCGCACTGCTGAAATCCCTGCTGCGGAGCTGACTGCAGCCAAATC 3712455  
QY 322 ATTGCTGATGTCGACGAGCGTAAACCGCGAAGCCTTGCCCGCGGCTGACA 381  
DB 3712456 GTCCGCGAAGCCGCGGAGTGAACCGGTTCAAAAGCGAAGCCGCTTGCCCATGCC 3712515  
QY 382 CCTGACTGTGAATACCGT 401  
DB 3712516 GCAGTGCTCCATCCCGGT 3712535

RESULT 11  
US-09-103-840A-2/c  
Sequence 2, Application US/09103840A  
Patent No. 6294328  
GENERAL INFORMATION:  
APPLICANT: FLEISCHMAN, Robert D.  
APPLICANT: WHITE, Owen R.  
APPLICANT: FRASER, Claire M.

APPLICANT: VENTER, John C.  
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM  
FILE REFERENCE: 24366-2007.00  
CURRENT APPLICATION NUMBER: US/09/103,840A  
CURRENT FILING DATE: 1998-06-24  
NUMBER OF SEQ ID NOS: 2  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 2  
LENGTH: 4403765  
TYPE: DNA  
ORGANISM: Mycobacterium tuberculosis  
FEATURE:  
OTHER INFORMATION: CDC 1551  
OTHER INFORMATION: "n" bases at various positions throughout the sequence  
OTHER INFORMATION: represent a, t, c or g  
US-09-103-840A-2

Query Match 2.6%; Score 34.2; DB 3; Length 4403765;  
Best Local Similarity 52.4%; Pred. No. 56;  
Matches 75; Conservative 0; Mismatches 68; Indels 0; Gaps 0;

QY 176 GCGCAACCTGCGCGGTAATACTGGTGAAGTGAACCGCGGCTGAGTGAATGCGCT 235  
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QY 236 ATCTGACATTAATGAGCGTCAAGCTGTGATAGCCGAGATTCTGCTTAATGCGCT 295  
DB 3381065 GCTCCGCGCTTTGTGCGCGACGACACTTGTGCGGTGCGGTGCGGTGCGGTGCG 3381006  
QY 296 GCGCGGAGTGTGTCAAGTGC 318  
DB 3381005 CGCGGACGCTGCGGTGCG 3380983

RESULT 12

US-09-103-840A-1/c  
Sequence 1, Application US/09103840A  
Patent No. 6294328  
GENERAL INFORMATION:  
APPLICANT: FLEISCHMAN, Robert D.  
APPLICANT: WHITE, Owen R.  
APPLICANT: FRASER, Claire M.  
APPLICANT: VENTER, John C.  
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM  
FILE REFERENCE: 24366-2007.00  
CURRENT APPLICATION NUMBER: US/09/103,840A  
CURRENT FILING DATE: 1998-06-24  
NUMBER OF SEQ ID NOS: 2  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 1  
LENGTH: 4411529  
TYPE: DNA  
ORGANISM: Mycobacterium tuberculosis  
OTHER INFORMATION: H37Rv  
US-09-103-840A-1

Query Match 2.6%; Score 34.2; DB 3; Length 4411529;  
Best Local Similarity 52.4%; Pred. No. 56;  
Matches 75; Conservative 0; Mismatches 68; Indels 0; Gaps 0;

QY 176 GCGCAACCTGCGCGGTAATACTGGTGAAGTGAACCGCGGCTGAGTGAATGCGCT 235  
DB 3385432 GCGCGCCGCTGACGACCACTCCGTTGACATATACCACTGACGACCGCTGACG 3385373  
QY 236 ATCTGACATTAATGAGCGTCAAGCTGTGATAGCCGAGATTGCTGCTTAATGCGCT 295  
DB 3385372 GCTCCGCGCTTTGTGCGCGACGACACTTGTGCGGTGCGGTGCGGTGCGGTGCG 3385313  
QY 296 GCGCGGAGTGTGTCAAGTGC 318  
DB 3385312 CGCGGACGCTGCGGTGCG 3385290

**Tue May 4 07:05:31 2004**

us-09-866-379d-9.rni

Page 8

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RESULT 13
US-07-885-089B-5/c
; Sequence 5, Application US/07885089B
; Patent No. 5830995
GENERAL INFORMATION:
APPLICANT: Shoyad, Mohammed
APPLICANT: McDonald, Vicki L.
APPLICANT: Bradley, James G.
APPLICANT: Plowman, Gregory D.
TITLE OF INVENTION: AMPHIREGLUTINS: A FAMILY OF
TITLE OF INVENTION: HEPARIN-BINDING EPITHELIAL CELL GROWTH FACTORS
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/885,089B
FILING DATE: 18-MAY-1992
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Cornuzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 5624-174
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
TELEFAX: 212-869-9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 998 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..744
US-07-885-089B-5
Query Match 2.6%; Score 34; DB 2; Length 998;
Best Local Similarity 56.1%; Pred. No. 0.51;
Matches 64; Conservative 0; Mismatches 50; Indels 0; Gaps 0
OY 4 AAAGCATCTTAATCCCATTTTATCTCTTCGATCCGCTAACCCCGCATTCGATTC 63
DB 510 AAMGTAATCTTGATGCAATGATGATGTCACACCCGAGTTCTGATGATTCGATTC 451
OY 64 GCTCAGATGAGCGCGAGCTGAAGCTGAAAGCTGTGATGTTCAGTGCAT 117
DB 450 GCCATGATCCAAAAGTTCTGAAACCTGCGACATGATGATTCCTTTCTTCTT 397
RESULT 14
US-09-621-976-8976
; Sequence 8976, Application US/09621976
; Patent No. 6639063
GENERAL INFORMATION:
APPLICANT: Dumas, Mhine Edwards, J.B.
APPLICANT: Jobert, S.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: ESTs and Encoded Human Proteins.
FILE REFERENCE: GENSET.054PR2

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CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.jp
SEQ ID NO 8976
LENGTH: 399
TYPE: DNA
ORGANISM: Homo sapiens
US-09-621-976-8976

Query Match      2.6%  Score 33.8; DB 4; Length 399;
Best Local Similarity 10.6%; Pred. No. 0.34; Mismatches 163; Indels 0; Gaps 0
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QY      517 TCAATTCGCACTTAAACGGGCAATTATCAACGCGCTTTCGCAACGGAACGGGTGCTT 576
      70 WGMATKMGKGRBAASWAGTSMWMTYMRKRYTYRRKCACTKRRRAAGMKGAMAWA 129
QY      577 AATTTTCGCAATCAAACTGTGTGCTTAAACGTGAAGAAACGACGAACTGTCAATTA 636
      130 KMWYAMRRTATKRYAMWMSKRSWBRRAWYMMYMARRYMGMAASCYRDAYAASG 189
QY      637 AGCGAGGACTTACCACTCGGAAGTCAAGGTGAGCGCGACTGTGTCTCATTAACGGTGG 696
      190 MYTMMYTMKRRKMYTSAGMSMRKRYRCAISYCSMSYCMGAKMMYMKTSRMSYYS 249
QY      697 GTAAGCTCGCATCAATGCTGACGAGATATTTCTCTGCAACAGACAGGAAATCCG 756
      250 SYCTCYRRSCCCMSGSCWYKTYYSWYCAICYSYTKKASCCMCCMKRRMAAMMY 309
QY      757 GACCGGGGTGGGGGAAGATCCAGATTCACACAGCAGTGAACAACCTGTGAATTG 813
      310 MMATYCKKTSAMRYRSCYSKMRMRMCMCAIMMTGSMWMCWTGTGGCTATTG 366

RESULT 15
US-08-680-326-116/c
Sequence 116, Application US/08680326
Patent No. 5925733
GENERAL INFORMATION:
APPLICANT: ROSE, TIMOTHY M.
APPLICANT: BOSCH, MARITX
APPLICANT: STRAND, KURT
APPLICANT: TODARO, GEORGE J.
TITLE OF INVENTION: DNA POLYMERASE OF GAMMA HERPES VIRUSES
TITLE OF INVENTION: ASSOCIATED WITH KAPOSI'S SARCOMA AND RETROPERITONEAL
NUMBER OF SEQUENCES: 152
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/680,326
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Schliff, J. Michael
REGISTRATION NUMBER: 40,253
REFERENCE/DOCKET NUMBER: 29938-20001.00
TELECOMMUNICATION INFORMATION:

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Tue May 4 07:05:30 2004

US-09-866-379d-7.rmpb

Page 1

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

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Listing first 45 summaries

Database : Published Applications NA:\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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4	1898.4	99.9	1901	9	US-09-866-379-9
5	1895.2	99.7	1901	9	US-09-866-379-6
6	1440.2	75.8	1486	16	US-10-284-962-4
7	1397.4	73.5	1489	15	US-10-266-041-9
8	1397.4	73.5	1489	16	US-10-284-962-1
9	1398	68.3	1289	13	US-10-282-122A-1167
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12	1287.8	67.7	1323	15	US-10-034-985-1
13	1287.8	67.7	1323	16	US-10-430-356-1
14	1263.8	66.5	1308	15	US-10-156-660-1

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17	466	24.5	466	13	US-10-282-122A-3181	Sequence 3, Appli
18	299.4	15.7	2181	13	US-10-282-122A-20324	Sequence 20324, A
19	229.2	12.1	1326	13	US-10-282-122A-41608	Sequence 41608, A
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22	222.4	11.7	254	16	US-10-317-444-302	Sequence 302, App
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24	222.4	11.7	254	16	US-10-317-444-304	Sequence 304, App
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26	211.4	11.1	1326	15	US-10-021-723A-11	Sequence 11, Appli
27	158	8.3	1431	15	US-10-021-723A-9	Sequence 9, Appli
28	111.4	5.9	1282	13	US-10-282-122A-19198	Sequence 19198, A
29	107.6	5.7	2160	13	US-10-282-122A-22963	Sequence 22963, A
30	101.4	5.3	2160	13	US-10-282-122A-39913	Sequence 39913, A
31	100.2	5.3	2199	13	US-10-282-122A-20408	Sequence 20408, A
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33	68	3.6	2232	13	US-10-282-122A-13362	Sequence 13362, A
34	64.8	3.4	1266	15	US-10-021-723A-5	Sequence 5, Appli
35	62.4	3.3	2202	13	US-10-282-122A-13620	Sequence 13620, A
36	61.4	3.2	2238	13	US-10-282-122A-13665	Sequence 13665, A
37	58.8	3.1	2220	13	US-10-282-122A-12931	Sequence 12931, A
38	56.8	3.0	11710	15	US-10-240-689-40	Sequence 40, Appli
39	55.2	2.9	2337	9	US-09-934-899-7	Sequence 7, Appli
40	55.2	2.9	2337	9	US-09-934-868-27	Sequence 27, Appli
41	55.2	2.9	2337	15	US-10-353-456-7	Sequence 7, Appli
42	55.2	2.9	2337	15	US-10-353-456-7	Sequence 7, Appli
43	51.4	2.7	5738	8	US-08-781-986A-84	Sequence 84, Appli
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## ALIGNMENTS

RESULT 1  
US-09-866-379-7  
Sequence 7, Application US/09866379  
Patent No. US20020136754A1  
GENERAL INFORMATION: SHORT, Jay  
APPLICANT: DIVERSA CORPORATION  
APPLICANT: KREITZ, Keith  
APPLICANT: BARTON, Nelson  
APPLICANT: GARETT, James  
APPLICANT: O'DONOGHUE, Eileen  
TITLE OF INVENTION: RECOMBINANT BACTERIAL PHYTASES AND USES THEREOF  
FILE REFERENCE: DIVER1370-7  
CURRENT APPLICATION NUMBER: US/09/866,379  
PRIOR FILING DATE: 2001-05-24  
PRIOR APPLICATION NUMBER: US 09/580,515  
PRIOR FILING DATE: 2000-05-25  
PRIOR APPLICATION NUMBER: US 09/318,528  
PRIOR FILING DATE: 1999-05-25  
PRIOR APPLICATION NUMBER: US 09/291,931  
PRIOR FILING DATE: 1999-04-13  
PRIOR APPLICATION NUMBER: US 09/259,214  
PRIOR FILING DATE: 1999-03-01  
PRIOR APPLICATION NUMBER: US 08/910,798  
PRIOR FILING DATE: 1997-08-13  
NUMBER OF SEQ ID NOS: 10  
SOFTWARE: Patentin version 3.1  
SEQ ID NO 7  
LENGTH: 1901  
TYPE: DNA  
ORGANISM: Escherichia coli  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (1)..(1901)  
OTHER INFORMATION: n is any nucleotide  
US-09-866-379-7

Query Match 99.9%; Score 1900; DB 9; Length 1901;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1901; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 241 ATCTGCAATTCGCTAGAGTAGCCGAGAGCTGAAAGCTGAAAAGTGTGTGATGTCAGTGC 300
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QY 301 TCATGATGTCGTCCTCCAAACCAAGGCGACGCACTGATGAGAGATGTCACCCCAAGCGC 360
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QY 361 ATGCGCAACCTGCGCGGTTAAACTGGTGTGCTACACCGCGNCTGTGATGATGATCGC 420
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QY 1201 CAATGAGACGCTTCGCGGTGACGCGGATTAACAGCGCGCAAGTGTGATCTGTGTTGA 1260
DB 1201 CAATGAGACGCTTCGCGGTGACGCGGATTAACAGCGCGCAAGTGTGATCTGTGTTGA 1260
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DB 1261 AGCTGGCGTGGCTTAACCGCAATTAACGCAAGTGAATCAGGTTTGGCTGGCTTCAAGAC 1320
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DB 1381 ACTGACCTCTGGAGATGTGAAGAGCGAATGCGAGGCGATGTGTGTGTGAGGATTT 1440
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DB 1621 TATTAACCGTAATGATTAAGCGGTAAGCGGCTGTGCGCGGTTAATCAACAT 1680
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DB 1741 CTTCTTTGCGGTTGTTCAAGCCAAAACGCGCAACGAGGCTGTGCAACAGAACGCC 1800
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DB 1801 CCAAGACCGCGGATTAATCAACCGCGCAAGTGTGAGGAGGATGATGATGATGATGATG 1860
QY 1861 AATGATGCTTGCCTTCAAGTCAATTAATGATGATGATGATGATGATGATGATGATG 1901
DB 1861 AATGATGCTTGCCTTCAAGTCAATTAATGATGATGATGATGATGATGATGATGATG 1901

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RESULT 2  
 US-10-156-660-3  
 ; Sequence 3, Application US/10156660  
 ; Publication No. US20030103958A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Short, Jay M.  
 ; APPLICANT: Kretz, Keith  
 ; APPLICANT: Gray, Kevin A.  
 ; APPLICANT: Barton, Nelson R.  
 ; APPLICANT: Garrett, James B.  
 ; APPLICANT: O'Donoghue, Eileen  
 ; APPLICANT: Mathur, Eric U.

TITLE OF INVENTION: PHYLASES, NUCLEIC ACIDS ENCODING THEM  
 TITLE OF INVENTION: AND METHODS FOR MAKING AND USING THEM  
 FILE REFERENCE: 09010-029007  
 CURRENT APPLICATION NUMBER: US/10/156,660  
 CURRENT FILING DATE: 2002-10-01  
 PRIOR APPLICATION NUMBER: US 09/866,379  
 PRIOR FILING DATE: 2001-05-24  
 PRIOR APPLICATION NUMBER: US 09/580,515  
 PRIOR FILING DATE: 2000-05-25  
 PRIOR APPLICATION NUMBER: US 09/318,528  
 PRIOR FILING DATE: 1999-05-25  
 PRIOR APPLICATION NUMBER: US 09/291,931  
 PRIOR FILING DATE: 1999-04-13  
 PRIOR APPLICATION NUMBER: US 09/259,214  
 PRIOR FILING DATE: 1999-03-01  
 PRIOR APPLICATION NUMBER: US 08/910,798  
 PRIOR FILING DATE: 1997-08-13  
 NUMBER OF SEQ ID NOS: 4  
 SOFTWARE: FastSeq for Windows Version 4.0  
 SEQ ID NO: 3  
 LENGTH: 1901  
 TYPE: DNA  
 ORGANISM: Escherichia coli  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: (188)...(1483)  
 FEATURE:  
 NAME/KEY: misc\_feature  
 LOCATION: 403  
 OTHER INFORMATION: n = A,T,C or G  
 US-10-156-660-3

Query Match 99.9%; Score 1900; DB 15; Length 1901;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1901; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 1381 ACTGACCTGCGGAGATGTAAGAGCGAATGCGGAGGATGTTTCTGTTGCAAGTTT 1440  
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Db 1621 TATACCGTAATAGTATAGCCCTAAGTGAAGCGGTGCGGCGGTTTATACACCAAT 1680  
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QY 1861 AATGTCGTTCGCGCGCATTCAGTAATTTAGCGCATTCGATCG 1901  
Db 1861 AATGTCGTTCGCGCGCATTCAGTAATTTAGCGCATTCGATCG 1901

## RESULT 3

US-09-866-379-5  
Sequence 5, Application US/09866379  
Patent No. US20020136754A1  
GENERAL INFORMATION:  
APPLICANT: DIVERSA CORPORATION  
APPLICANT: SHORT, Jay  
APPLICANT: KRETZ, Keith  
APPLICANT: GRAY, Kevin  
APPLICANT: BARTON, Nelson  
APPLICANT: GARRETT, James  
APPLICANT: O'DONOGHUE, Eileen  
TITLE OF INVENTION: RECOMBINANT BACTERIAL PHYTASES AND USES THEREOF  
FILE REFERENCE: DIVER1370-7  
CURRENT APPLICATION NUMBER: US/09/866,379  
PRIOR FILING DATE: 2001-05-24  
PRIOR APPLICATION NUMBER: US 09/580,515  
PRIOR FILING DATE: 2000-05-25  
PRIOR APPLICATION NUMBER: US 09/318,528  
PRIOR FILING DATE: 1999-05-25  
PRIOR APPLICATION NUMBER: US 09/291,931  
PRIOR FILING DATE: 1999-04-13  
PRIOR APPLICATION NUMBER: US 09/259,214  
PRIOR FILING DATE: 1999-03-01  
PRIOR APPLICATION NUMBER: US 08/910,798  
PRIOR FILING DATE: 1997-08-13  
NUMBER OF SEQ ID NOS: 10  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 5  
LENGTH: 1901  
TYPE: DNA  
ORGANISM: Escherichia coli  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (1)..(1901)  
OTHER INFORMATION: n is any nucleotide  
US-09-866-379-5

Query March 99.9%; Score 1898.4; DB 9; Length 1901;  
Best local similarity 99.9%; Pred. No. 0;  
Matches 1900; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
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Db 1201 CAATGGAAGCTTCCCGGTCAGCGCGGATTAACAGCGCGCGCGCGCGCGCGCGCGCG 1260  
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Db 1261 ACCGTGGCGTCGAGTAAAGCATTAAACAGCAAGTATTCAGTTTCCTTCAGAC 1320  
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Db 1321 TTTTACAGCAATGCTGATATAAAAGCCGCTGCTTAAATACCCGCCGAGAGTGA 1380  
Qy 1381 ACTGACCTGAGCAAGATGTGAAGAGCAAAATGCGAGAGCATGTGCTTGGCAGTTT 1440  
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Db 1861 AATGCTGCTTGGCCATTCAGTAATGACGATCCGATCG 1901

RESULT 4  
US-09-866-379-9  
Sequence 9, Application US/09866379  
Patent No. US20020136754A1  
GENERAL INFORMATION:  
APPLICANT: DIVERSA CORPORATION  
APPLICANT: SHORT, Jay  
APPLICANT: KREITZ, Keith  
APPLICANT: GRAY, Kevin  
APPLICANT: BARTON, Nelson  
APPLICANT: GARRETT, James  
APPLICANT: O'DONOGHUE, Eileen  
TITLE OF INVENTION: RECOMBINANT BACTERIAL PHYTASES AND USES THEREOF  
FILE REFERENCE: DIVERL370-7  
CURRENT APPLICATION NUMBER: US/09/866,379  
CURRENT FILING DATE: 2001-05-24  
PRIOR APPLICATION NUMBER: US 09/580,515  
PRIOR FILING DATE: 2000-05-25  
PRIOR APPLICATION NUMBER: US 09/318,528  
PRIOR FILING DATE: 1999-05-25  
PRIOR APPLICATION NUMBER: US 09/291,931  
PRIOR FILING DATE: 1999-04-13  
PRIOR APPLICATION NUMBER: US 09/259,214  
PRIOR FILING DATE: 1998-03-01  
PRIOR APPLICATION NUMBER: US 08/910,798  
PRIOR FILING DATE: 1997-08-13  
NUMBER OF SEQ ID NOS: 10  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 9

LENGTH: 1901  
TYPE: DNA  
ORGANISM: Escherichia coli  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (1)-(1901)  
OTHER INFORMATION: n is any nucleotide  
US-09-866-379-9

Query Match 99.9%; Score 1898.4; DB 9; Length 1901;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1900; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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 Db 901 GCTGACGAGATATTTCTCTGCAACAAGGATATCCGAGACCGGGTGGGAG 960  
 QY 961 GATCAACGATTCACACAGTGGAAACCTTGTGTAAGTTGCAATAAGCGCAATTTTATTT 1020  
 Db 961 GATCAACGATTCACACAGTGGAAACCTTGTGTAAGTTGCAATAAGCGCAATTTTATTT 1020  
 QY 1021 GCTACACGACGACGAGTGGTGGCGGACCGCGGACCGCGTATTAATGATTTGATCA 1080  
 Db 1021 GCTACACGACGACGAGTGGTGGCGGACCGCGGACCGCGTATTAATGATTTGATCA 1080  
 QY 1081 GACAGCGTTCAGCGCCCATTCACCGCAAAAAGCGATGGTGTGACATTAACCACTTC 1140  
 Db 1081 GACAGCGTTCAGCGCCCATTCACCGCAAAAAGCGATGGTGTGACATTAACCACTTC 1140  
 QY 1141 AGTGTGTTTATTCGCGGACAGATCTAATCTGGAATTCGCGGAGCGGACCTGAGCT 1200  
 Db 1141 AGTGTGTTTATTCGCGGACAGATCTAATCTGGAATTCGCGGAGCGGACCTGAGCT 1200  
 QY 1201 CAAGTGAAGCTTCCCGGTGACCGGATTAACGCGCCGAGGTGATGAATGATTTTGA 1260  
 Db 1201 CAAGTGAAGCTTCCCGGTGACCGGATTAACGCGCCGAGGTGATGAATGATTTTGA 1260  
 QY 1261 AGCGTGGCTGCGCTTAAGGATTAACGCGCATTCAGGTTTGGTGTCTCTTCCAGAC 1320  
 Db 1261 AGCGTGGCTGCGCTTAAGGATTAACGCGCATTCAGGTTTGGTGTCTCTTCCAGAC 1320  
 QY 1321 TTATACAGCAGATTCGATTAACGCGCGCTGATTAATACCGCCCGGAGAGGTGA 1380  
 Db 1321 TTATACAGCAGATTCGATTAACGCGCGCTGATTAATACCGCCCGGAGAGGTGA 1380  
 QY 1381 ACTGACCTTGGCAGATGTGAAGGAAATGCGCAGGGCATGTGTTGTTGGCAGGTTT 1440  
 Db 1381 ACTGACCTTGGCAGATGTGAAGGAAATGCGCAGGGCATGTGTTGTTGGCAGGTTT 1440  
 QY 1441 TAGCAAAATGTAATGAAGACAGCATACCGGCGTCAAGTTTGAATGCAATAAAAGAG 1500  
 Db 1441 TAGCAAAATGTAATGAAGACAGCATACCGGCGTCAAGTTTGAATGCAATAAAAGAG 1500  
 QY 1501 CATTCAGTTACCTGAATGCTCTGAGGCTGATGAACAAACGAAAGCTGTAAATGCGTGA 1560  
 Db 1501 CATTCAGTTACCTGAATGCTCTGAGGCTGATGAACAAACGAAAGCTGTAAATGCGTGA 1560  
 QY 1561 CCGGAAAAGCGCTTCAAGCGCATTCGCGCACTTCAAGTTTCTCTTCTCGAGGTAAC 1620  
 Db 1561 CCGGAAAAGCGCTTCAAGCGCATTCGCGCACTTCAAGTTTCTCTTCTCGAGGTAAC 1620  
 QY 1621 TATTAACGTAATGATTAAGCCTGAATCTGTAGCGGTGCGGCTTTAATGACACAT 1680  
 Db 1621 TATTAACGTAATGATTAAGCCTGAATCTGTAGCGGTGCGGCTTTAATGACACAT 1680  
 QY 1681 TGAAGATAGGCGCTTTAATTAATGACGCTGCTGTTCAAGCGTCAATGAACAACTCA 1740  
 Db 1681 TGAAGATAGGCGCTTTAATTAATGACGCTGCTGTTCAAGCGTCAATGAACAACTCA 1740  
 QY 1741 CTTCTTTGGGCGGTTCGAAGCAAAAGCGCAACAGCAAGGCTGTGCAACGAAAGCGC 1800  
 Db 1741 CTTCTTTGGGCGGTTCGAAGCAAAAGCGCAACAGCAAGGCTGTGCAACGAAAGCGC 1800  
 QY 1801 CCAAGACGCGGCGATCACTCAAGCGCAGCATCGCGCGGCTGATGAACATCAAGATCGT 1860  
 Db 1801 CCAAGACGCGGCGATCACTCAAGCGCAGCATCGCGCGGCTGATGAACATCAAGATCGT 1860  
 QY 1861 AATGTCGTTGCGCCATTCAGTAATGAAGCATCCGATCG 1901  
 Db 1861 AATGTCGTTGCGCCATTCAGTAATGAAGCATCCGATCG 1901

RESULT 5  
 US-09-866-379-6  
 ; Sequence 6, Application US/09866379  
 ; Patent No. US20020136754A1

; GENERAL INFORMATION:  
 ; APPLICANT: DIVERSA CORPORATION  
 ; APPLICANT: SHORT, Jay  
 ; APPLICANT: KRETZ, Keith  
 ; APPLICANT: GRAY, Kevin  
 ; APPLICANT: BARTON, Nelson  
 ; APPLICANT: GARRETT, James  
 ; APPLICANT: O'DONOGHUE, Eileen  
 ; TITLE OF INVENTION: RECOMBINANT BACTERIAL PHYTASES AND USES THEREOF  
 ; FILE REFERENCE: DIVER1370-7  
 ; CURRENT APPLICATION NUMBER: US/09/866,379  
 ; CURRENT FILING DATE: 2001-05-24  
 ; PRIOR APPLICATION NUMBER: US 09/580,515  
 ; PRIOR FILING DATE: 2000-05-25  
 ; PRIOR APPLICATION NUMBER: US 09/318,528  
 ; PRIOR FILING DATE: 1999-05-25  
 ; PRIOR APPLICATION NUMBER: US 09/291,931  
 ; PRIOR FILING DATE: 1999-04-13  
 ; PRIOR APPLICATION NUMBER: US 09/259,214  
 ; PRIOR FILING DATE: 1999-03-01  
 ; PRIOR APPLICATION NUMBER: US 08/910,798  
 ; PRIOR FILING DATE: 1997-08-13  
 ; NUMBER OF SEQ ID NOS: 10  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 6  
 ; LENGTH: 1901  
 ; TYPE: DNA  
 ; ORGANISM: Escherichia coli  
 ; FEATURE:  
 ; NAME/KEY: misc feature  
 ; LOCATION: (1)..(1901)  
 ; OTHER INFORMATION: n is any nucleotide  
 US-09-866-379-6

Query Match 99.7%; Score 1895.2; DB 9; Length 1901;  
 Best Local Similarity 99.8%; Pred. No. 0;  
 Matches 1898; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TAAAGGAGAAAGAAATGATGATTTAATCTTGTGCTGCGCAATTTTGTGATGTTG 60  
 Db 1 TAAAGGAGAAAGAAATGATGATTTAATCTTGTGCTGCGCAATTTTGTGATGTTG 60  
 QY 61 CTCTCCACCTTGTGTGTGATGATGCTGAGACCGCGCTGTGAAAAGTTTACGAGTAC 120  
 Db 61 CTCTCCACCTTGTGTGTGATGATGCTGAGACCGCGCTGTGAAAAGTTTACGAGTAC 120  
 QY 121 TGAATGCGGCGATTAAGCATGCGATCAGGCAATCAATATGTCAGATATGAAAAGCGGAAA 180  
 Db 121 TGAATGCGGCGATTAAGCATGCGATCAGGCAATCAATATGTCAGATATGAAAAGCGGAAA 180  
 QY 181 CATATCATGAAAGCATCTTAATCCGATTTTATCTTTCTGATTCGTTAACCCCGCA 240  
 Db 181 CATATCATGAAAGCATCTTAATCCGATTTTATCTTTCTGATTCGTTAACCCCGCA 240  
 QY 241 ATCTGCATTCGCTCAGATGAGTGGCGGAGCTGGAAGCTGAAAAGTGTGATGTGCAATG 300  
 Db 241 ATCTGCATTCGCTCAGATGAGTGGCGGAGCTGGAAGCTGAAAAGTGTGATGTGCAATG 300  
 QY 241 ATCTGCATTCGCTCAGATGAGTGGCGGAGCTGGAAGCTGAAAAGTGTGATGTGCAATG 300  
 Db 241 ATCTGCATTCGCTCAGATGAGTGGCGGAGCTGGAAGCTGAAAAGTGTGATGTGCAATG 300  
 QY 301 TCATGATGCTGCTGCTCAACCAAGGCGCAAGCTGATGAGAGATGACCCGAGCGC 360  
 Db 301 TCATGATGCTGCTGCTCAACCAAGGCGCAAGCTGATGAGAGATGACCCGAGCGC 360  
 QY 361 ATGGCCAACTTGGCGCGTAAACTGGGTTGCTCAACCGGAGGTGTGAGCTTAATGCG 420  
 Db 361 ATGGCCAACTTGGCGCGTAAACTGGGTTGCTCAACCGGAGGTGTGAGCTTAATGCG 420  
 QY 421 CTAATCTGGAATTAACCAAGCCGAGCTGTGTGAGCGAGCTGCTGCGGAGAAAAGGG 480  
 Db 421 CTAATCTGGAATTAACCAAGCCGAGCTGTGTGAGCGAGCTGCTGCGGAGAAAAGGG 480  
 QY 481 CTGCGCGAGTGTGCTCAGTGTGCGGATTAATGCTGATGTGAGAGAGTACCCGTAAC 540  
 Db 481 CTGCGCGAGTGTGCTCAGTGTGCGGATTAATGCTGATGTGAGAGAGTACCCGTAAC 540

QY 541 AGCGAAGCCTTGGCCGCGGCTGCACTGACTGCAATAACGTACATACCAAGC 600  
 DB 541 AGCGAAGCCTTGGCCGCGGCTGCACTGACTGCAATAACGTACATACCAAGC 600  
 QY 601 AGATACGTCAAGTCCGATCCGTTATTTAAATCTCTAAAAATGGCGCTTGGCACTGA 660  
 DB 601 AGATACGTCAAGTCCGATCCGTTATTTAAATCTCTAAAAATGGCGCTTGGCACTGA 660  
 QY 661 TAAAGCGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 720  
 DB 661 TAAAGCGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 720  
 QY 721 CGGGGATCGGCAACCGCGCTTGGCACTGCAAGCGGCTGAATTTTTCGCAATCAAA 780  
 DB 721 CGGGGATCGGCAACCGCGCTTGGCACTGCAAGCGGCTGAATTTTTCGCAATCAAA 780  
 QY 781 CTGTGCTTAAACGTGAAGAAACAGACGAAAGCTGTTCAATTAACGCAATTAACATC 840  
 DB 781 CTGTGCTTAAACGTGAAGAAACAGACGAAAGCTGTTCAATTAACGCAATTAACATC 840  
 QY 841 GGAATCTAAGGTGAAGCGCGCAATGCTCAATTAACGCGTGGTAAAGCTCGCATCAAT 900  
 DB 841 GGAATCTAAGGTGAAGCGCGCAATGCTCAATTAACGCGTGGTAAAGCTCGCATCAAT 900  
 QY 901 GCTGACGAGATATTTCTCTGCAACAGCAAGGAAATGCGGAGCGCGGCTGGGAG 960  
 DB 901 GCTGACGAGATATTTCTCTGCAACAGCAAGGAAATGCGGAGCGCGGCTGGGAG 960  
 QY 961 GATCACCATTTCAACCAAGTGAAGCACTTGTGAATTTGATTAACGGCAATTTATTT 1020  
 DB 961 GATCACCATTTCAACCAAGTGAAGCACTTGTGAATTTGATTAACGGCAATTTATTT 1020  
 QY 1021 GCTACAAAGCAAGCGGAGGTTGCGCGAGCGCGCAAGCGCGGCTGATTTGATCA 1080  
 DB 1021 GCTACAAAGCAAGCGGAGGTTGCGCGAGCGCGCAAGCGCGGCTGATTTGATCA 1080  
 QY 1081 GACAGCGTTGACGCGGCTTCAACCGGCAAAACAGCGGCTGATTTGATTTGATTTG 1140  
 DB 1081 GACAGCGTTGACGCGGCTTCAACCGGCAAAACAGCGGCTGATTTGATTTGATTTG 1140  
 QY 1141 AGTGTGTTTATCGCGGCAAGATATCTGCAATCTCGGCGCGCATGAGACT 1200  
 DB 1141 AGTGTGTTTATCGCGGCAAGATATCTGCAATCTCGGCGCGCATGAGACT 1200  
 QY 1201 CAATGAGAGCTTCCCGGTGAGCGCGGATTAACCGCGCGGCTGATTTGATTTGATTTG 1260  
 DB 1201 CAATGAGAGCTTCCCGGTGAGCGCGGATTAACCGCGCGGCTGATTTGATTTGATTTG 1260  
 QY 1261 AGCTGAGAGCTTCCCGGTGAGCGCGGATTAACCGCGCGGCTGATTTGATTTGATTTG 1320  
 DB 1261 AGCTGAGAGCTTCCCGGTGAGCGCGGATTAACCGCGCGGCTGATTTGATTTGATTTG 1320  
 QY 1321 TTTACAGAGATGCTGATTAACCGCGGCTGATTTGATTTGATTTGATTTGATTTG 1380  
 DB 1321 TTTACAGAGATGCTGATTAACCGCGGCTGATTTGATTTGATTTGATTTGATTTG 1380  
 QY 1381 ACTGACCTGAGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1440  
 DB 1381 ACTGACCTGAGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1440  
 QY 1441 TACGCAAAATCGTAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1500  
 DB 1441 TACGCAAAATCGTAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1500  
 QY 1501 CATTCAGTTAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1560  
 DB 1501 CATTCAGTTAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1560  
 QY 1561 CGGGAAGAGCGGCTTCAAGCGGATCGGCGCACTTTCAATTTCTCTTCTGAGATAC 1620  
 DB 1561 CGGGAAGAGCGGCTTCAAGCGGATCGGCGCACTTTCAATTTCTCTTCTGAGATAC 1620

QY 1621 TATAACCGTAATAGTAAAGCGGTAAGCGGCTGCTGCGGCTTAAATCAACCAT 1680  
 DB 1621 TATAACCGTAATAGTAAAGCGGTAAGCGGCTGCTGCGGCTTAAATCAACCAT 1680  
 QY 1681 TGAAGATAGCGCTTAAATAGAGCGGCTGCTGCGGCTGCTGCGGCTTAAATAGAG 1740  
 DB 1681 TGAAGATAGCGCTTAAATAGAGCGGCTGCTGCGGCTGCTGCGGCTTAAATAGAG 1740  
 QY 1741 CCTCTTGGCGGCTTAAAGCGGCAACCGGCAACCGGCAACCGGCAACCGGCAACCGG 1800  
 DB 1741 CCTCTTGGCGGCTTAAAGCGGCAACCGGCAACCGGCAACCGGCAACCGGCAACCGG 1800  
 QY 1801 CCAAGACCGGCGGCTTAAAGCGGCAACCGGCAACCGGCAACCGGCAACCGGCAACCGG 1860  
 DB 1801 CCAAGACCGGCGGCTTAAAGCGGCAACCGGCAACCGGCAACCGGCAACCGGCAACCGG 1860  
 QY 1861 AATGATGCTGCGGCTTAAAGCGGCAACCGGCAACCGGCAACCGGCAACCGGCAACCGG 1901  
 DB 1861 AATGATGCTGCGGCTTAAAGCGGCAACCGGCAACCGGCAACCGGCAACCGGCAACCGG 1901

## RESULT 6

US-10-284-962-4  
 ; Sequence 4: Application US/10284962  
 ; Publication No. US20030206913A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Webel, Douglas M.  
 ; APPLICANT: Orr, Donald E.  
 ; APPLICANT: Ruch, Frank E.  
 ; TITLE OF INVENTION: PHYTASE-CONTAINING ANIMAL FOOD AND METHOD  
 ; FILE REFERENCE: 834460-71725  
 ; CURRENT APPLICATION NUMBER: US/10/284,962  
 ; CURRENT FILING DATE: 2002-10-31  
 ; PRIOR APPLICATION NUMBER: US 60/335,303  
 ; PRIOR FILING DATE: 2001-10-31  
 ; NUMBER OF SEQ ID NOS: 14  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 4  
 ; LENGTH: 1486  
 ; TYPE: DNA  
 ; ORGANISM: Escherichia coli  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: (188) ..(1483)  
 ; OTHER INFORMATION:  
 US-10-284-962-4

## Query Match

75.8%; Score 1440.2; DB 16; Length 1486;  
 Best Local Similarity 98.0%; Pred. No. 0;  
 Matches 1457; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

QY 1 TAAAGAGCAAGAACATGATGATGATGATGATGATGATGATGATGATGATGATGATG 60  
 DB 1 TAAAGAGCAAGAACATGATGATGATGATGATGATGATGATGATGATGATGATGATG 60  
 QY 61 CTCTCCACCTTGT 120  
 DB 61 CTCTCCACCTTGT 120  
 QY 121 TGAATGGGCGGCTTAAAGCGGCAACCGGCAACCGGCAACCGGCAACCGGCAACCGG 180  
 DB 121 TGAATGGGCGGCTTAAAGCGGCAACCGGCAACCGGCAACCGGCAACCGGCAACCGG 180  
 QY 181 CATATGATGAAAGCGATCTTAATCCCATTTTATCTCTTGTATTCGTTAAACCGGCA 240  
 DB 181 CATATGATGAAAGCGATCTTAATCCCATTTTATCTCTTGTATTCGTTAAACCGGCA 240  
 QY 241 ATCTGATGCTCAGAGTGAAGCGGCAACCGGCAACCGGCAACCGGCAACCGGCAACCGG 300  
 DB 241 ATCTGATGCTCAGAGTGAAGCGGCAACCGGCAACCGGCAACCGGCAACCGGCAACCGG 300  
 QY 301 TCATGATGCTCAGAGTGAAGCGGCAACCGGCAACCGGCAACCGGCAACCGGCAACCGG 360

Db	301	TCACGTGTGTGGTGTCCCCCAACCAAGGACGCAACTGATGAGAGATGTCACCCCAAGCGC	360
QY	361	ATGGCCCAACCTGGCCGGGTAAAACTGTGGTGTGCTACACCCGGGAGTGGTGAATTCGC	420
Db	361	ATGGCCCAACCTGGCCGGGTAAAACTGTGGTGTGCTGACACCAAGCGAGTGTGACTTAATTCGC	420
QY	421	CTATCTCGGACATTTACCAACCGCCAGCGCTCTGTGTAGCCGACGGATTTGCTGGCGAAAAAGG	480
Db	421	CTATCTCGGACATTTACCAACCGCCAGCGCTGTGTGTAGCGGATTTGCTGGCGAAAAAGG	480
QY	481	CTGGCCCGCAGCTGTGTGACGCTGTGCGGATTTATTTGTCTGATGTGACACGAGCTACCGGTAAAC	540
Db	481	CTGGCCCGCAGCTGTGTGACGCTGTGCGGATTTATTTGTGATGTGACACGAGCTACCGGTAAAC	540
QY	541	AGGCGAAAGCCTTCGCGCGCGGAGCTTGACACTGACTGTGCATTAACCGTACATAACCGGC	600
Db	541	AGGCGAAAGCCTTCGCGCGGAGCTTGACACTGACTGTGCATTAACCGTACATAACCGAGGC	600
QY	601	AGATACGCGCAGTCCCGATTCGGTATTTAATTCCTCTAAACCTGGCGTTTGGCCAACTGGA	660
Db	601	AGATACGCTCAGTCCCGATTCGGTATTTAATTCCTCTAAACCTGGCGTTTCCCACTGGA	660
QY	661	TAAACGCGACGTGACTGACGCGATCTCTAGCAGAGGCGAGAGGTCATTTGTGACTTTAC	720
Db	661	TAAACGCGACCTGTACTGACGCGATCTCTAGCAGAGGCGAGAGGTCATTTGTGACTTTAC	720
QY	721	CGGGCATTCGGCAAAACGGGGTTTCGCGAACGTGGAACGGGTGTGTAATTTTCGCAATCAA	780
Db	721	CGGGCATTCGGCAAAACGGGGTTTCGCGAACGTGGAACGGGTGTGTAATTTTTCGCAATCAA	780
QY	781	CTTGTGCTTTAAACGTGAGAAACAGAGCGAAAGCTGTCATTTAACGACGACATTAACATC	840
Db	781	CTTGAACCTTTAAACGTGAGAAACAGAAATGAAGCTGTACTTTAACGACGACATTAACATC	840
QY	841	GGAACTCAAGGTGAGCGCGCGCAATGTCTCACTTAAACGGGTGGGTAACCTCGCATCAAT	900
Db	841	GGAACTCAAGGTGAGCGCGCGCAATGTCTCACTTAAACGGGTGGGTAACCTCGCATCAAT	900
QY	901	GCTGACGAGATATTTCTCTTGCAACAAGCAAGGAATGCCGAGCCGGGGTGGGAAG	960
Db	901	GCTGACGGAATATTTCTCTTGCAACAAGCAAGGAATGCCGAGCCGGGGTGGGAAG	960
QY	961	GATCAACGATTTCAACCCAGTGGAAACACTTGTCTAATTTGATTAACCGGCATTTTATTT	1020
Db	961	GATCACTATTTCAACCCAGTGGAAACACTTGTCTAATTTGATTAACCGGCATTTTATTT	1020
QY	1021	GCTAACACGCAACGCCAGAGTTTGCCCGACGCCGCCACCCCGTTATTGAATTGATCAA	1080
Db	1021	ACTACAAACGCAACGCCAGAGTTTGCCCGACAGTCGCCCAACCCCGTTATTGATTTGATCAA	1080
QY	1081	GACAGCGTGTGACGCCCATCCACCGCAAAAACAGCGATATGTGTGACATTAACCACTTC	1140
Db	1081	GACAGCGTGTGACGCCCATCCACCGCAAAAACAGCGATATGTGTGACATTAACCACTTC	1140
QY	1141	AGTGTGTTTATTCGCCGGAACAACGATATCTAATCTGCAAAATCTCGCGGCGCACTGAGACT	1200
Db	1141	AGTGTGTTTATTCGCCGGAACAACGATATCTAATCTGCAAAATCTCGCGGCGCACTGAGACT	1200
QY	1201	CAACTGACGCTTCGCCGTCAGCCGAGTAAACGCGCGCAAGGTGTGAACCTGGTGTGA	1260
Db	1201	CAACTGACGCTTCGCCAGTTCAGCCGAGTAAACGCGCGCAAGGTGTGAACCTGGTGTGA	1260
QY	1261	ACGCTGCGCTCGGCTTAAGCGATTAACGCAAGTGAATTCAGGTTTGCTGTCTTCACAGC	1320
Db	1261	ACGCTGCGCTCGGCTTAAGCGATTAACGCAAGTGAATTCAGGTTTGCTGTCTTCACAGC	1320
QY	1321	TTTACAGCAGATGTCGTGATTAAAACCCGCTGCATTTAATACCGCCCGGAGAGGTGAA	1380
Db	1321	TTTACAGCAGATGTCGTGATTAAAACCCGCTGCATTTAATACCGCCCGGAGAGGTGAA	1380
QY	1381	ACTGACCTCTGGCAGATGTGAAAGCGAAATCGCAGGGCATGTGTCTGTGGCAGGTTT	1440
Db	1381	ACTGACCTCTGGCAGATGTGAAAGCGAAATCGCAGGGCATGTGTCTGTGGCAGGTTT	1440

QY	1441	TAGGCAATCGTGAATGAAGACCCATACCGCGGTGAGTTGTAA	1486
Db	1441	TACGCAATCGTGAATGAAGACCCCATACCGCGGTGAGTTGTAA	1486
<p>RESULT 7 US-10-266-041-9 ; Sequence 9, Application US/10266041 ; Publication No. US20030072844A1 ; GENERAL INFORMATION: ; APPLICANT: Lei, Xingen ; TITLE OF INVENTION: ENZYMES WITH IMPROVED PHYTASE ACTIVITY ; FILE REFERENCE: 19603/2791 ; CURRENT APPLICATION NUMBER: US/10/266, 041 ; CURRENT FILING DATE: 2002-10-07 ; PRIOR APPLICATION NUMBER: US/09/540,149 ; PRIOR FILING DATE: 2000-03-31 ; PRIOR APPLICATION NUMBER: 60/127, 032 ; PRIOR FILING DATE: 1999-03-31 ; NUMBER OF SEQ ID NOS: 9 ; SOFTWARE: PatentIn Ver. 2.1 ; SEQ ID NO 9 ; LENGTH: 1489 ; TYPE: DNA ; ORGANISM: Escherichia coli US-10-266-041-9</p>			
QY		Query Match 73.5%; Score 1397.4; DB 15; Length 1489; Best Local Similarity 97.1%; Pred. No. 0; Matches 1445; Conservative 0; Mismatches 37; Indels 6; Gaps 2	
QY	1	TAAAGGACGAAACCAATGCTGATTTACTTTGTTCTGTCGCAATTTTGTGATGTGTCG	60
Db	1	TAAAGGACGAAACCAATGCTGATTTCTTTGTTCTGTCGCAATTTGATGTGTCG	60
QY	61	CTCTCCACCTTGTGTGTGATGCTGACCCCGCTGAAAATTACGAACGTAGCC	120
Db	61	CTCTCCACCTTGTGTGTGATGCTGACCCCGGATTAAGAAATTACGAACGTAGCC	120
QY	121	TGATGGCGGCGATTAGCATCGATAGGCATGAAATGTGAGATTAAGAAAGCGAAA	180
Db	121	TGATGGCGGCGATTAGCATCGATAGGCATGAAATGTGAGATTAAGAAAGCGAAA	180
QY	121	TGATGGCGGCGATTAGCATCGATAGGCATGAAATGTGAGATTAAGAAAGCGAAA	174
QY	181	CATATCGATGAAGCGATTTATCCATTTTATCTCTTCTGATTCGGTTAACCCCGCA	240
Db	175	CATATCGATGAAGCGATTTATCCATTTTATCTCTTCTGATTCGGTTAACCCCGCA	234
QY	241	ATCTGCATTCGCTCAAGGTGAGCCGGAAGCTGAAGCTGAAAAGTGTGTATTCACGTG	300
Db	235	ATCTGCATTCGCTCAAGGTGAGCCGGAAGCTGAAGCTGAAAAGTGTGTATTCACGTG	294
QY	301	TCAATGATGAGCGTCCCAACCAAGGCGCAACGCACTGATCAGGATGTCAACCCAGACG	360
Db	295	TCAATGATGAGCGTCCCAACCAAGGCGCAACGCACTGATCAGGATGTCAACCCAGACG	354
QY	361	ATGAGCAACTGCGCGGTAAATCTGGGTTGCTGACACCGGAGGTGTGATGATTCG	420
Db	355	ATGAGCAACTGCGCGGTAAATCTGGGTTGCTGACACCGGAGGTGTGATGATTCG	414
QY	421	CTATCTCGGACATTACCAACGCGCAGCGTCTGGTAGCGGACGAGATTTGTGCGAAAAAGG	480
Db	415	CTATCTCGGACATTACCAACGCGCAGCGTCTGGTAGCGGACGAGATTTGTGCGAAAAAGG	474
QY	481	CTGCGCGCACTGTGTCAGGTGCGCATTTATGTCGATGTGACGAGCGTACCCGTAAAC	540
Db	475	CTGCGCGCACTGTGTCAGGTGCGCATTTATGTCGATGTGACGAGCGTACCCGTAAAC	534
QY	541	AGGCGAAGCCTTGCGCGCGCGGCTGCGACCTGATCTGTGCAATTAACGCTACATACCAAGGC	600
Db	535	AGGCGAAGCCTTGCGCGCGCGGCTGCGACCTGATCTGTGCAATTAACGCTACATACCAAGGC	594
QY	601	AGATAGCTTCAGTCCGATTCGGTATTATTAATCTCTTAATAATCTGCGGTTGCCAATCGA	660

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Db 595 AGATACGTCCAGTCCGATCCGTTATTTATCTCTTAAATCGCGTTGCCAATCGA 654
Qy 661 TAAACGGAAAGTGAAGTGAAGGATCTCAGAGGGGAGAGGGTCAATGCTGACTTAC 720
Db 655 TAAACGGAAAGTGAAGTGAAGGATCTCAGAGGGGAGAGGGTCAATGCTGACTTAC 714
Qy 721 CGAGCATCGGCAAAAGCGGTTTGGCGAAGTGAAGCGGGTCTTAATTTTCCGATCAAA 780
Db 715 CGAGCATCGGCAAAAGCGGTTTGGCGAAGTGAAGCGGGTCTTAATTTTCCGATCAAA 774
Qy 781 CTTGTGCTTTAAAGTGAAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 840
Db 775 CTTGTGCTTTAAAGTGAAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 834
Qy 841 GGAACCTAAGGTGAGCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 900
Db 835 GGAACCTAAGGTGAGCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 894
Qy 901 GCTGACGGAAGATATTTCTCTGCAACAGAGAGAGAGAGAGAGAGAGAGAGAGAG 960
Db 895 GCTGACGGAAGATATTTCTCTGCAACAGAGAGAGAGAGAGAGAGAGAGAGAGAG 954
Qy 961 GATACCGGATTCACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1020
Db 955 GATACCGGATTCACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1014
Qy 1021 GCTCAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1080
Db 1015 ACTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1074
Qy 1081 GACAGCGTGAAGCGCCCATCCAGCGCAAAAGAGAGAGAGAGAGAGAGAGAGAG 1140
Db 1075 GACAGCGTGAAGCGCCCATCCAGCGCAAAAGAGAGAGAGAGAGAGAGAGAGAG 1134
Qy 1141 AGTCTGTTTATGCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1200
Db 1135 AGTCTGTTTATGCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1194
Qy 1201 CAACCTGAGCGTTCCGAGTACCGAGATTAACGCGCGAGAGAGAGAGAGAGAG 1260
Db 1195 CAACCTGAGCGTTCCGAGTACCGAGATTAACGCGCGAGAGAGAGAGAGAGAG 1254
Qy 1261 ACAGTGCAGTGCAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1320
Db 1255 ACAGTGCAGTGCAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1314
Qy 1321 TTACAGCAGATGCGTGAATTAACGCGCGTGTCAATTAATACGCGCGAGAGAG 1380
Db 1315 TTACAGCAGATGCGTGAATTAACGCGCGTGTCAATTAATACGCGCGAGAGAG 1374
Qy 1381 ACTGACCTTGGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1440
Db 1375 ACTGACCTTGGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1434
Qy 1441 TACGCAATGCTGAATGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1488
Db 1435 TACGCAATGCTGAATGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1482

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RESULT 8
US-10-284-962-1
; Sequence 1, Application US/10284962
; Publication No. US20030206913A1
; GENERAL INFORMATION:
; APPLICANT: Weibel, Douglas M.
; APPLICANT: Orr, Donald E.
; APPLICANT: Ruch, Frank E.
; TITLE OF INVENTION: PHYTASE-CONTAINING ANIMAL FOOD AND METHOD
; FILE REFERENCE: 834460-71725
; CURRENT APPLICATION NUMBER: US/10/284,962
; CURRENT FILING DATE: 2002-10-31
; PRIOR APPLICATION NUMBER: US 60/335,303

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; PRIOR FILING DATE: 2001-10-31
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1489
; TYPE: DNA
; ORGANISM: Escherichia coli
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: (1)..(22)
; OTHER INFORMATION:
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: (1468)..(1489)
; OTHER INFORMATION:
; NAME/KEY: CDS
; LOCATION: (16)..(108)
; OTHER INFORMATION:
; NAME/KEY: CDS
; LOCATION: (182)..(1480)
; OTHER INFORMATION:
US-10-284-962-1

Query Match 73.5%; Score 1397.4; DB 16; Length 1489;
Best Local Similarity 97.1%; Pred. No. 0;
Matches 1445; Conservative 0; Mismatches 37; Indels 6; Gaps 2;

Qy 1 TAAAGGAGAGAAAGATGATTTACTTTGTTGCGGCAATTTGTGATGTTGCG 60
Db 1 TAAAGGAGAGAAAGATGATTTACTTTGTTGCGGCAATTTGTGATGTTGCG 60
Qy 61 CTCTCACCTTGTGTTGATGATGCTGAGACCGCGCTGAAAAGTTAAAGAGAGCC 120
Db 61 CTCTCACCTTGTGTTGATGATGCTGAGACCGCGCTGAAAAGTTAAAGAGAGCC 120
Qy 121 TGAATGCGGCTTGAAGATGATGATGATGATGATGATGATGATGATGATGATG 180
Db 121 TGAATGCGGCTTGAAGATGATGATGATGATGATGATGATGATGATGATGATG 180
Qy 181 CATATGATGAAGAGATCTTAATCCATTTTAACTCTTGATTCCTGTTAACCCGCA 240
Db 175 CATATGATGAAGAGATCTTAATCCATTTTAACTCTTGATTCCTGTTAACCCGCA 234
Qy 241 ATCTGATTCGCTCAGAGTGAAGCGAGCTGAAGCTGAAAAGTGTGATGATGATG 300
Db 235 ATCTGATTCGCTCAGAGTGAAGCGAGCTGAAGCTGAAAAGTGTGATGATGATG 294
Qy 301 TCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 360
Db 295 TCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 354
Qy 361 ATGCGCAACTGCGCGGTTAAATCTGTTGCTGACACCGGAGTGTGATGATGATG 420
Db 355 ATGCGCAACTGCGCGGTTAAATCTGTTGCTGACACCGGAGTGTGATGATGATG 414
Qy 421 CTATGCGGAGATTAACAGAGCAGAGCTGATGATGATGATGATGATGATGATGATG 480
Db 415 CTATGCGGAGATTAACAGAGCAGAGCTGATGATGATGATGATGATGATGATGATG 474
Qy 481 CTGCGCGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 540
Db 475 CTGCGCGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 534
Qy 541 AGCGGAGGCTTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 600
Db 535 AGCGGAGGCTTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 594
Qy 601 AGATAGTCAATGCGGATCCGTTATTTAATCTGTTAAATCTGCGGTTGCGAACTG 660
Db 595 AGATAGTCAATGCGGATCCGTTATTTAATCTGTTAAATCTGCGGTTGCGAACTG 654

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Qy 661 TAACGCGAAGCTGACGCGGATCTTCAGCAGGCGAGGATCAATTGCTGACCTTAC 720
Db 655 TAACGCGAAGCTGACGCGGATCTTCAGCAGGCGAGGATCAATTGCTGACCTTAC 724
Qy 721 CGGGCATCGCGAAGCGGCTTCCGGAACCTGGAACGGGTGCTTAATTTCCGCAATCAA 780
Db 715 CGGGCATCGCGAAGCGGCTTCCGGAACCTGGAACGGGTGCTTAATTTCCGCAATCAA 774
Qy 781 CTGTGCTTAAAGCTGAGAAACAGAACGAAAGCTGTTCAATTAACGAGCATTAACATC 840
Db 775 CTGTGCTTAAAGCTGAGAAACAGAACGAAAGCTGTTCAATTAACGAGCATTAACATC 834
Qy 841 GGAATCTAAGGTGAGCGCGCAATGCTCTTAACCGGTGCGGTAAAGCTCCGATCAAT 900
Db 835 GGAATCTAAGGTGAGCGCGCAATGCTCTTAACCGGTGCGGTAAAGCTCCGATCAAT 894
Qy 901 GCTGACGAGATATTTCTCTGCAACAGCAGGGAATGCGGAGCGGCGGTGGAG 960
Db 895 GCTGACGAGATATTTCTCTGCAACAGCAGGGAATGCGGAGCGGCGGTGGAG 954
Qy 961 GATCAGCATTCACACGAGTGAACACTTGTCTAAGTTGATACCGCATTTATTT 1020
Db 955 GATCAGCATTCACACGAGTGAACACTTGTCTAAGTTGATACCGCATTTATTT 1014
Qy 1021 GCTACAAACGACGACGAGGTTGCCGAGCGCGCCACCCGTTATTAGATTGATCAA 1080
Db 1015 ACTACAAACGACGACGAGGTTGCCGAGCGCGCCACCCGTTATTAGATTGATCAT 1074
Qy 1081 GACAGCGTTGACGCCCCATCCACCGCAAAAACGGCGTATGCTGACATTACCACTTC 1140
Db 1075 GACAGCGTTGACGCCCCATCCACCGCAAAAACGGCGTATGCTGACATTACCACTTC 1134
Qy 1141 AGTGTGTTTATCGCGGACACGAACTAATCTGGCAAAATCGCGCGGCGCATGAGCT 1200
Db 1135 AGTGTGTTTATCGCGGACACGAACTAATCTGGCAAAATCTGGCGGCGCATGAGCT 1194
Qy 1201 CAAGTGAACGCTTCCCGGTGACCGCGATTAACAGCGCGCGAGGTGATGTTGA 1260
Db 1195 CAAGTGAACGCTTCCCGGTGACCGCGATTAACAGCGCGCGAGGTGATGTTGA 1254
Qy 1261 ACGTGGCGTGGCTTAAGCGATTAACAGCGAGTGAATTAAGTTGCTGCTCCAGAC 1320
Db 1255 ACGTGGCGTGGCTTAAGCGATTAACAGCGAGTGAATTAAGTTGCTGCTCCAGAC 1314
Qy 1321 TTTAACGAGATGCTGATTAATAACCGCGCTGTCTTAATAACCGCGCGGAGAGTGA 1380
Db 1315 TTTAACGAGATGCTGATTAATAACCGCGCTGTCTTAATAACCGCGCGGAGAGTGA 1374
Qy 1381 ACTGACCCCTGAGAGATGTAAGAGCGGAAATGCGGAGGCAATGCTGCTGAGAGTTT 1440
Db 1375 ACTGACCCCTGAGAGATGTAAGAGCGGAAATGCGGAGGCAATGCTGCTGAGAGTTT 1434
Qy 1441 TAACGAAATCGTGAATGAAGACGCAATCCGCGCTGCAAGTTGTAATG 1488
Db 1435 TAACGAAATCGTGAATGAAGAGCGCATCCGCGCTGCAAGTTGTAATG 1482

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## RESULT 9

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US-10-282-122A-7167
; Sequence 7167, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:

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; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselebeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.

```

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; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; PENDING FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 7167
; LENGTH: 1299
; TYPE: DNA
; ORGANISM: Escherichia coli
US-10-282-122A-7167

Query Match 68.3%; Score 1298; DB 13; Length 1299;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1298; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 188 ATGAAAGCATCTTAATCCATTTTATCTCTGATTCGTTAACCCTGATCTGCA 247
Db 1 ATGAAAGCATCTTAATCCATTTTATCTCTGATTCGTTAACCCTGATCTGCA 60
Qy 248 TTGCTCAAGTGAAGCGGAGCTGAAGCTGGAAGTGTGATGATGCTGATGCT 307
Db 61 TTGCTCAAGTGAAGCGGAGCTGAAGCTGGAAGTGTGATGATGCTGATGCT 120
Qy 308 GTGCGTCTCAACCAAGCGCAACGCAATGATGACAGATGACACCCAGCATGCGCA 367
Db 121 GTGCGTCTCAACCAAGCGCAACGCAATGATGACAGATGACACCCAGCATGCGCA 180
Qy 368 ACTGCGCGGTAAACTGGGTGCTGACACCGCGAGGTGTGAGCTTAATGCTATCTC 427
Db 181 ACTGCGCGGTAAACTGGGTGCTGACACCGCGAGGTGTGAGCTTAATGCTATCTC 240
Qy 428 GGAATTAACCAACGCGAGGCTGAGTGAAGCGGAGATGCTGCGGAAAAAGGGCTGCCG 487
Db 241 GGAATTAACCAACGCGAGGCTGAGTGAAGCGGAGATGCTGCGGAAAAAGGGCTGCCG 300
Qy 488 CAGTCTGTCAGGTGCGATTAATGCTGATGTCAGACAGCGTAAACCGTAAACAGGCGAA 547
Db 301 CAGTCTGTCAGGTGCGATTAATGCTGATGTCAGACAGCGTAAACCGTAAACAGGCGAA 360
Qy 548 GCTTGGCGCGCGGCGTGGCACTGATGTAATTAACCTGATCAATACCGAGGAGATAG 607
Db 361 GCTTGGCGCGCGGCGTGGCACTGATGTAATTAACCTGATCAATACCGAGGAGATAG 420
Qy 608 TCCAGTCCGATCCGTTATTAATCTCTAATAACTGGGCTTGGCAACTGATTAACCGG 667
Db 421 TCCAGTCCGATCCGTTATTAATCTCTAATAACTGGGCTTGGCAACTGATTAACCGG 480
Qy 668 AACGTGACGAGCGGATCTCTGACAGGAGGAGGATCAATGCTGATTAACCGGCGAT 727
Db 481 AACGTGACGAGCGGATCTCTGACAGGAGGAGGATCAATGCTGATTAACCGGCGAT 540

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QY 728 CGGCAAGCGGCTTTCGGAACTGAAAGGCTTATTTTCCGCAATCAACTTGGC 787  
DB 541 CGGCAAGCGGCTTTCGGAACTGAAAGGCTTATTTTCCGCAATCAACTTGGC 600  
QY 788 CTTAAACGTGAGAAACGAGCAAGAGCTGTTCAATTACGAGCAATTCACATCGAACTC 847  
DB 601 CTTAAACGTGAGAAACGAGCAAGAGCTGTTCAATTACGAGCAATTCACATCGAACTC 660  
QY 848 AAGGTGAGCGCGCAATATGTTCTCATTTAACCGGTGCGTTAAGCTTCGATCATGTGACG 907  
DB 661 AAGGTGAGCGCGCAATATGTTCTCATTTAACCGGTGCGTTAAGCTTCGATCATGTGACG 720  
QY 908 GAGATATTTCTCTGCAACGAGCAAGGGAATGCGGAGCGGAGTGGGGAAGATCACG 967  
DB 721 GAGATATTTCTCTGCAACGAGCAAGGGAATGCGGAGCGGAGTGGGGAAGATCACG 780  
QY 968 GATTCAACCAAGTGAACACCTTGTAAAGTTGATTAACGCGCAATTTTATTGCTACAA 1027  
DB 781 GATTCAACCAAGTGAACACCTTGTAAAGTTGATTAACGCGCAATTTTATTGCTACAA 840  
QY 1028 CGCAAGCGGAGGTTGCGCGAGCGCGCGCAACCGGTTATTGATTTGATTAAGCAAGCG 1087  
DB 841 CGCAAGCGGAGGTTGCGCGAGCGCGCGCAACCGGTTATTGATTTGATTAAGCAAGCG 900  
QY 1088 TTGACGCGCCCATCAACCGCAAAACAGGCGTATGTTGACATTAACCACTTCACTGCTG 1147  
DB 901 TTGACGCGCCCATCAACCGCAAAACAGGCGTATGTTGACATTAACCACTTCACTGCTG 960  
QY 1148 TTATATCGCGGACAGATTAATCTGGAATCTTCGCGCGGCGCATCTGAGCTCACTGCG 1207  
DB 961 TTATATCGCGGACAGATTAATCTGGAATCTTCGCGCGGCGCATCTGAGCTCACTGCG 1020  
QY 1208 AGCTTCGCGGTCAGCGGATTAACGCGCGGCGGATGGAATCTGTTTGAAGCTGCG 1267  
DB 1021 AGCTTCGCGGTCAGCGGATTAACGCGCGGCGGATGGAATCTGTTTGAAGCTGCG 1080  
QY 1268 CGTGGCGCTTAAGGATTAACGCGGATGGAATCTGTTTGAAGCTGCG 1327  
DB 1081 CGTGGCGCTTAAGGATTAACGCGGATGGAATCTGTTTGAAGCTGCG 1140  
QY 1328 GAGATGCGGATTAACGCGGCTGATTAATTAAGCGCGCGGAGAGTGAATGACG 1387  
DB 1141 GAGATGCGGATTAACGCGGCTGATTAATTAAGCGCGCGGAGAGTGAATGACG 1200  
QY 1388 CTGGGAGATGTAAGAGGAAATGCGGAGGCGATGTTGCTTGGCAAGTTTACGCA 1447  
DB 1201 CTGGGAGATGTAAGAGGAAATGCGGAGGCGATGTTGCTTGGCAAGTTTACGCA 1260  
QY 1448 ATCGTGAATGAAGCAACGATACCGGCGTGCAGTTTGTAA 1486  
DB 1261 ATCGTGAATGAAGCAACGATACCGGCGTGCAGTTTGTAA 1299

RESULT 10  
US-09-777-566A-1  
Sequence 1, Application US/0977566A  
Patent No. US20010055788A1  
GENERAL INFORMATION:  
APPLICANT: DIVERSA CORPORATION  
APPLICANT: SHORT, Jay  
APPLICANT: KREIZ, Keith  
TITLE OF INVENTION: RECOMBINANT BACTERIAL PHYTASES AND USES THEREOF  
FILE REFERENCE: DIVER1370-6  
CURRENT APPLICATION NUMBER: US/09/777,566A  
CURRENT FILING DATE: 2001-06-11  
PRIOR APPLICATION NUMBER: US 09/318,528  
PRIOR FILING DATE: 1999-05-25  
PRIOR APPLICATION NUMBER: US 09/291,931  
PRIOR FILING DATE: 1999-04-13  
PRIOR APPLICATION NUMBER: US 09/259,214  
PRIOR FILING DATE: 1999-03-01  
PRIOR APPLICATION NUMBER: US 08/910,798

PRIOR FILING DATE: 1997-08-13  
NUMBER OF SEQ ID NOS: 4  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 1  
LENGTH: 1323  
ORGANISM: Escherichia coli  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (1)..(1320)  
NAME/KEY: misc\_feature  
LOCATION: (1)..(1323)  
OTHER INFORMATION: n is any nucleotide  
US-09-777-566A-1

Query Match 67.7%; Score 1287.8; DB 9; Length 1323;  
Best Local Similarity 99.5%; Pred. No. 0;  
Matches 1293; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 188 ATGAAAGCATCTTAATCCATTTTATCTTCTGATTCGTTAACCCCGCAATCTGCA 247  
DB 1 ATGAAAGCATCTTAATCCATTTTATCTTCTGATTCGTTAACCCCGCAATCTGCA 60  
QY 248 TTGCTTCAGATGAGCGCGAGAGCTGAAAGCTGAAAGCTGATTTGATTTGATTTGATTT 307  
DB 61 TTGCTTCAGATGAGCGCGAGAGCTGAAAGCTGAAAGCTGATTTGATTTGATTTGATTT 120  
QY 308 GTGCTGCTCAACCAAGGCGCAAGCTGATGACAGATGTCACCCGCAAGCTGCA 367  
DB 121 GTGCTGCTCAACCAAGGCGCAAGCTGATGACAGATGTCACCCGCAAGCTGCA 180  
QY 368 ACTGCGCGGTAAACTGGGTTGCTGCAACGCGGAGTGTGATTTATCGCTATCTC 427  
DB 181 ACTGCGCGGTAAACTGGGTTGCTGCAACGCGGAGTGTGATTTATCGCTATCTC 240  
QY 428 GGAATTACCAAGCGGAGCTGATGAGCGAGATGCGGAGATGCGGAGGCTGCGG 487  
DB 241 GGAATTACCAAGCGGAGCTGATGAGCGAGATGCGGAGATGCGGAGGCTGCGG 300  
QY 488 CAGTGTGATGAGTGTGATTTATGCTGATGTCAGAGCGTACCGGTAAACAGCGCA 547  
DB 301 CAGTGTGATGAGTGTGATTTATGCTGATGTCAGAGCGTACCGGTAAACAGCGCA 360  
QY 548 GCTTGGCGCGCGGCTGCGAAGCTGATGCTGCAATTAACGTTACATCCAGGAGATAG 607  
DB 361 GCTTGGCGCGCGGCTGCGAAGCTGATGCTGCAATTAACGTTACATCCAGGAGATAG 420  
QY 608 TCCAGTCCCATCCGTTATTTAATCTCTAATAAACTGCGGTTTCCCACTGATTAACGCG 667  
DB 421 TCCAGTCCCATCCGTTATTTAATCTCTAATAAACTGCGGTTTCCCACTGATTAACGCG 480  
QY 668 AAGCTGATCAACGAGTCTCAGAGAGGCGAGAGGCTCAATTTGCTGATTTACCGGCAAT 727  
DB 481 AAGCTGATCAACGAGTCTCAGAGAGGCGAGAGGCTCAATTTGCTGATTTACCGGCAAT 540  
QY 728 CGGCAAGCGGCTTTCGCAACGAGCAAGGAGTCTTAATTTTCCGCAATCAACTTGTGCG 787  
DB 541 CGGCAAGCGGCTTTCGCAACGAGCAAGGAGTCTTAATTTTCCGCAATCAACTTGTGCG 600  
QY 788 CTTAAACGTGAGAAACGAGCAAGAGCTGTTCAATTACGAGCAATTTACATCGAACTC 847  
DB 601 CTTAAACGTGAGAAACGAGCAAGAGCTGTTCAATTACGAGCAATTTACATCGAACTC 660  
QY 848 AAGGTGAGCGCGCAATATGTTCTCATTTAACCGGTGCGTTAAGCTTCGATCATGTGACG 907  
DB 661 AAGGTGAGCGCGCAATATGTTCTCATTTAACCGGTGCGTTAAGCTTCGATCATGTGACG 720  
QY 908 GAGATATTTCTCTGCAACGAGCAAGGGAATGCGGAGCGGAGTGGGGAAGATCACG 967  
DB 721 GAGATATTTCTCTGCAACGAGCAAGGGAATGCGGAGCGGAGTGGGGAAGATCACG 780  
QY 968 GATTCAACCAAGTGAACACCTTGTAAAGTTGATTAACGCGCAATTTTATTGCTACAA 1027

DB 781 GATTACACCAAGTGAACACCTGTAAGTTGATTAACGCAATTTATTTGTAACA 840  
QY 1028 CGCAGCGCAAGAGTTGGCCCGCAGCCGCGCCACCCCTTATTAATTTGATCAAGACGCG 1087  
DB 841 CGCAGCGCAAGAGTTGGCCCGCAGCCGCGCCACCCCTTATTAATTTGATCAAGACGCG 900  
QY 1088 TTGACGCGCCCATCCACCGCAAAAACAGGCGTATGTTGACATTAACCACTTCAAGTCTG 1147  
DB 901 TTGACGCGCCCATCCACCGCAAAAACAGGCGTATGTTGACATTAACCACTTCAAGTCTG 960  
QY 1148 TTATTCGCGGACACGATTAATCTGCAATTTCCGCGCGCGCATCTGAGGCTCACTG 1207  
DB 961 TTATTCGCGGACACGATTAATCTGCAATTTCCGCGCGCGCATCTGAGGCTCACTG 1020  
QY 1208 ACAGTTCGCGGACACGATTAATCTGCAATTTCCGCGCGCGCATCTGAGGCTCACTG 1267  
DB 1021 ACAGTTCGCGGACACGATTAATCTGCAATTTCCGCGCGCGCATCTGAGGCTCACTG 1080  
QY 1268 CGTCGCGGACACGATTAATCTGCAATTTCCGCGCGCGCATCTGAGGCTCACTG 1327  
DB 1081 CGTCGCGGACACGATTAATCTGCAATTTCCGCGCGCGCATCTGAGGCTCACTG 1140  
QY 1328 CAGATTCGCGGACACGATTAATCTGCAATTTCCGCGCGCGCATCTGAGGCTCACTG 1387  
DB 1141 CAGATTCGCGGACACGATTAATCTGCAATTTCCGCGCGCGCATCTGAGGCTCACTG 1200  
QY 1388 CTGGCAGGATGTAAGACGCAATTCGCGGCGCATGTTGTTGGAGGTTTTCGCA 1447  
DB 1201 CTGGCAGGATGTAAGACGCAATTCGCGGCGCATGTTGTTGGAGGTTTTCGCA 1260  
QY 1448 ATCGGATGTAAGACGCAATTCGCGGCGCATGTTGTTGGAGGTTTTCGCA 1487  
DB 1261 ATCGGATGTAAGACGCAATTCGCGGCGCATGTTGTTGGAGGTTTTCGCA 1300

RESULT 11  
US-09-866-379-1  
Sequence 1, Application US/09866379  
Patent No. US20020136754A1  
GENERAL INFORMATION:  
APPLICANT: DIVERSA CORPORATION  
APPLICANT: SHORT, Jay  
APPLICANT: KREIZ, Keith  
APPLICANT: GRAY, Kevin  
APPLICANT: BARTON, Nelson  
APPLICANT: GARRETT, James  
APPLICANT: O'DONOGHUE, Eileen  
TITLE OF INVENTION: RECOMBINANT BACTERIAL PHYTASES AND USES THEREOF  
FILE REFERENCE: DIVER1370-7  
CURRENT APPLICATION NUMBER: US/09/866,379  
PRIOR FILING DATE: 2001-05-24  
PRIOR APPLICATION NUMBER: US 09/580,515  
PRIOR FILING DATE: 2000-05-25  
PRIOR APPLICATION NUMBER: US 09/318,528  
PRIOR FILING DATE: 1999-05-25  
PRIOR APPLICATION NUMBER: US 09/291,931  
PRIOR FILING DATE: 1999-04-13  
PRIOR APPLICATION NUMBER: US 09/259,214  
PRIOR FILING DATE: 1999-03-01  
PRIOR APPLICATION NUMBER: US 08/910,798  
PRIOR FILING DATE: 1997-08-13  
NUMBER OF SEQ ID NOS: 10  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 1  
LENGTH: 1323  
TYPE: DNA  
ORGANISM: Escherichia coli  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (1)..(1323)  
OTHER INFORMATION: n is any nucleotide  
NAME/KEY: CDS  
LOCATION: (1)..(1323)

OTHER INFORMATION:  
US-09-866-379-1  
Query Match 67.7%; Score 1287.8; DB 9; Length 1323;  
Best Local Similarity 99.5%; Pred. No. 0; Mismatches 7; Indels 0; Gaps 0;  
Matches 1293; Conservative 0; Mismatches 7; Indels 0; Gaps 0;  
QY 188 ATGAAGGAGATCTTAATCCATTTTATCTCTGATTCGCTTAACCCGCAATCTGCA 247  
DB 1 ATGAAGGAGATCTTAATCCATTTTATCTCTGATTCGCTTAACCCGCAATCTGCA 60  
QY 248 TTGCGTCAAGTGAAGCCGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 307  
DB 61 TTGCGTCAAGTGAAGCCGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 120  
QY 308 GTGCGTCTCAACCAAGGCGCAAGCACTGATGCAAGATGCAACCCAGACGATGCGCA 367  
DB 121 GTGCGTCTCAACCAAGGCGCAAGCACTGATGCAAGATGCAACCCAGACGATGCGCA 180  
QY 368 ACCTGACCGGTAAACTGGGTGCTGACACCCGCGGTGAGTGAAGTGAAGTGAAGTGAAGT 427  
DB 181 ACCTGACCGGTAAACTGGGTGCTGACACCCGCGGTGAGTGAAGTGAAGTGAAGTGAAGT 240  
QY 428 GGCATTTACCAAGCAGCGTCTGTAAGCGAGATTTGTCGCAAAAAGGCGTGGCCG 487  
DB 241 GGCATTTACCAAGCAGCGTCTGTAAGCGAGATTTGTCGCAAAAAGGCGTGGCCG 300  
QY 488 CAGTCTGTCAGTGGCGATTATTTGCTGATGTCGACGAGCGTAAACCGTAAACAGCGCA 547  
DB 301 CAGTCTGTCAGTGGCGATTATTTGCTGATGTCGACGAGCGTAAACCGTAAACAGCGCA 360  
QY 548 GCCTTGGCGCGGCGGTGGCACTGATGTCGATTAACCGTAAACCGTAAACAGCGCA 607  
DB 361 GCCTTGGCGCGGCGGTGGCACTGATGTCGATTAACCGTAAACCGTAAACAGCGCA 420  
QY 608 TCCAGTCCCGATCCGTTATTTATCTCTAAACCTGCGCTTGGCACTGATTAACCGG 667  
DB 421 TCCAGTCCCGATCCGTTATTTATCTCTAAACCTGCGCTTGGCACTGATTAACCGG 480  
QY 668 AACGTACTGACGCGATCTCAGACGAGGAGGATCAATTGCTGAACCGGCGAT 727  
DB 481 AACGTACTGACGCGATCTCAGACGAGGAGGATCAATTGCTGAACCGGCGAT 540  
QY 728 CGGCAAAACGCGGTTTGGCACTGAAACGAGGCTTAATTTTCCGCAATCAACTGTCG 787  
DB 541 CGGCAAAACGCGGTTTGGCACTGAAACGAGGCTTAATTTTCCGCAATCAACTGTCG 600  
QY 788 CTTAAACGTGAAGAAACAGACGAAAGCTGTCAATTAACGACGATTAACCGAATCTC 847  
DB 601 CTTAAACGTGAAGAAACAGACGAAAGCTGTCAATTAACGACGATTAACCGAATCTC 660  
QY 848 AAGGTAGGCGCGCAATGCTCATTAACCGGTGCGTAAGCTTCGATCAATGCTGACG 907  
DB 661 AAGGTAGGCGCGCAATGCTCATTAACCGGTGCGTAAGCTTCGATCAATGCTGACG 720  
QY 908 GAGATTTTCTCTGCAACAGACGAGGAATGCGGAGCCGCGGTGCGGAGGATCAC 967  
DB 721 GAGATTTTCTCTGCAACAGACGAGGAATGCGGAGCCGCGGTGCGGAGGATCAC 780  
QY 968 GATTACACCAAGTGAACCTTGTAGTTGATTAACGCGCAATTTATTTGCTACA 1027  
DB 781 GATTACACCAAGTGAACCTTGTAGTTGATTAACGCGCAATTTATTTGCTACA 840  
QY 1028 CGCAGCGCAAGTGTGCGCGCAGCCGCGCAACCCGTTATTTGATTTGAACAGGCG 1087  
DB 841 CGCAGCGCAAGTGTGCGCGCAGCCGCGCAACCCGTTATTTGATTTGAACAGGCG 900  
QY 1088 TTGACGCGCCCATCCACCGCAAAAACAGGCGTATGTTGACATTAACCACTTCAAGTCTG 1147  
DB 901 TTGACGCGCCCATCCACCGCAAAAACAGGCGTATGTTGACATTAACCACTTCAAGTCTG 960  
QY 1148 TTATTCGCGGACACGATTAATCTGCAATTTCCGCGCGCGCATCTGAGGCTCACTG 1207

Db 961 TTATATGCGGACACGATACCTAATCTGCAAAATCTCGGCGGCGACCTGAGCTCAACTGG 1020  
 QY 1208 ACGCTTCCCGGTGACGCGGATTAACACGCGCCAGGTGGTGAATCTGTGTTGAACGCTGG 1267  
 Db 1021 ACGCTTCCCGGTGACGCGGATTAACACGCGCCAGGTGGTGAATCTGTGTTGAACGCTGG 1080  
 QY 1268 CGTGGGCTTAAGGATTAACAGCAGTGAATTCAGTTGGCTGGTCTTCTTCAAGCTTAAAG 1327  
 Db 1081 CGTGGGCTTAAGGATTAACAGCAGTGAATTCAGTTGGCTGGTCTTCTTCAAGCTTAAAG 1140  
 QY 1328 CAGATGCGGTATTAACAGCAGTGAATTCAGTTGGCTGGTCTTCTTCAAGCTTAAAG 1387  
 Db 1141 CAGATGCGGTATTAACAGCAGTGAATTCAGTTGGCTGGTCTTCTTCAAGCTTAAAG 1200  
 QY 1388 CTGGGAGGATGTAAGAGGGAATGCGAGGGGAGTGTGGTGGGAGGTTTAAAGCAA 1447  
 Db 1201 CTGGGAGGATGTAAGAGGGAATGCGAGGGGAGTGTGGTGGGAGGTTTAAAGCAA 1260  
 QY 1448 ATCGTGAATGAAGACGACATACCGGCTGTCAGTTGGTAAAT 1487  
 Db 1261 ATCGTGAATGAAGACGACATACCGGCTGTCAGTTGGTAAAT 1300

RESULT 12  
 US-10-034-985-1  
 ; Sequence 1, Application US/10034985  
 ; Publication No. US2003004981S1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Kretz, Keith  
 ; TITLE OF INVENTION: NOVEL PHYTASE  
 ; FILE REFERENCE: 09010/029003  
 ; CURRENT APPLICATION NUMBER: US/10/034,985  
 ; PRIOR FILING DATE: 2001-12-21  
 ; PRIOR APPLICATION NUMBER: US/09/580,515  
 ; PRIOR FILING DATE: 1999-05-25  
 ; PRIOR APPLICATION NUMBER: 09/291,931  
 ; PRIOR FILING DATE: 1999-04-13  
 ; PRIOR APPLICATION NUMBER: 08/910,798  
 ; PRIOR FILING DATE: 1997-08-13  
 ; PRIOR APPLICATION NUMBER: 09/259,214  
 ; PRIOR FILING DATE: 1999-03-01  
 ; NUMBER OF SEQ ID NOS: 4  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 1  
 ; LENGTH: 1323  
 ; TYPE: DNA  
 ; ORGANISM: Escherichia coli  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: (1)...(1320)  
 ; NAME/KEY: misc\_feature  
 ; LOCATION: (1)...(1323)  
 ; OTHER INFORMATION: n = A,T,C or G  
 ; US-10-034-985-1

Query Match 67.7%; Score 1287.8; DB 15; Length 1323;  
 Best Local Similarity 99.5%; Pred. No. 0;  
 Matches 1293; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 188 ATGAAAGCATCTTAATCCCATTTTATCTCTTCTGATTCGTTAAACCCCGCAATCTGCA 247  
 Db 1 ATGAAAGCATCTTAATCCCATTTTATCTCTTCTGATTCGTTAAACCCCGCAATCTGCA 60  
 QY 248 TTGGGTCAGAGTGAAGCGGAGCTGAAGCTGGAAGGTGGTGAATCTGATGCTCATGGT 307  
 Db 61 TTGGGTCAGAGTGAAGCGGAGCTGAAGCTGGAAGGTGGTGAATCTGATGCTCATGGT 120  
 QY 308 GTGGGTCCTCAACCAAGGCGCAACTGATCAAGATCTCAACCCCAAGCGATGCGCA 367  
 Db 121 GTGGGTCCTCAACCAAGGCGCAACTGATCAAGATCTCAACCCCAAGCGATGCGCA 180  
 QY 368 ACCTGGCCGCTAAACCTGGGTTGGCTGACCGCGAGGTGGTGAATTCGCTATCTC 427

Db 181 ACCTGGCCGCTAAACCTGGGTTGGCTGACCGCGAGGTGGTGAATTCGCTATCTC 240  
 QY 428 GGAATTAACCAAGCGAGGCTCTGATAGCGGACGGAATGCTGCGCAAAAAGGGCTGCGCG 487  
 Db 241 GGAATTAACCAAGCGAGGCTCTGATAGCGGACGGAATGCTGCGCAAAAAGGGCTGCGCG 300  
 QY 488 CAGTGTGTCAGGTTCGATTAATGCTGATGTCAGAGACGTAACCCGTAACAGCGCA 547  
 Db 301 CAGTGTGTCAGGTTCGATTAATGCTGATGTCAGAGACGTAACCCGTAACAGCGCA 360  
 QY 548 GCCTTGGCCGCGGGCTGGGACCTGACTGTGCAATACCGTACATACCCAGGAGATAG 607  
 Db 361 GCCTTGGCCGCGGGCTGGGACCTGACTGTGCAATACCGTACATACCCAGGAGATAG 420  
 QY 608 TCCAGTCCCGATCGTTATTTAATCTCTTAAACCTGGGTTTCCCACTGATTAACGCG 667  
 Db 421 TCCAGTCCCGATCGTTATTTAATCTCTTAAACCTGGGTTTCCCACTGATTAACGCG 480  
 QY 668 AACGTGACTGACCGGATCTCTGACAGGCGAGAGGCTCAATTGCTGACTTTACCGGCAAT 727  
 Db 481 AACGTGACTGACCGGATCTCTGACAGGCGAGAGGCTCAATTGCTGACTTTACCGGCAAT 540  
 QY 728 CGGCAACCGGCTTTGCGCAACTGGAACGCGGCTTAATTTTCGCAATCAACTGCTGC 787  
 Db 541 CGGCAACCGGCTTTGCGCAACTGGAACGCGGCTTAATTTTCGCAATCAACTGCTGC 600  
 QY 788 CTTAAACGTGAGAAACAGACGAAAGCTTTCATTAACGAGGCAATTAACATCGAACTC 847  
 Db 601 CTTAAACGTGAGAAACAGACGAAAGCTTTCATTAACGAGGCAATTAACATCGAACTC 660  
 QY 848 AAGGTGAGCCCGCAATGCTCTCATTAACGAGGCGGTAACCTTCGATTAATGCTGACG 907  
 Db 661 AAGGTGAGCCCGCAATGCTCTCATTAACGAGGCGGTAACCTTCGATTAATGCTGACG 720  
 QY 908 GAGATATTTCTCCGCAACAGACAGAGGATCCGAGCGGAGTGGGAGAGATCAC 967  
 Db 721 GAGATATTTCTCCGCAACAGACAGAGGATCCGAGCGGAGTGGGAGAGATCAC 780  
 QY 968 GATTCAACCAAGTGAACACCTTGTCTAATGTTGCTAATACCGGCAATTTAATTGCTACAA 1027  
 Db 781 GATTCAACCAAGTGAACACCTTGTCTAATGTTGCTAATACCGGCAATTTAATTGCTACAA 840  
 QY 1028 CGCAGCGCAGAGGTTGGCCGCGAGCGGCGCACCCCGTTAATTTGATCAAGACAGCG 1087  
 Db 841 CGCAGCGCAGAGGTTGGCCGCGAGCGGCGCACCCCGTTAATTTGATCAAGACAGCG 900  
 QY 1088 TTGAACGCCCATCCACCGCAAAAACAGCGGTATGATGATTAACCCACTTCAGTACTG 1147  
 Db 901 TTGAACGCCCATCCACCGCAAAAACAGCGGTATGATGATTAACCCACTTCAGTACTG 960  
 QY 1148 TTATATGCGGAGCAAGTAACTAATCTGGAATCTGCGCGGCGCACTGAGACTCAACTGG 1207  
 Db 961 TTATATGCGGAGCAAGTAACTAATCTGGAATCTGCGCGGCGCACTGAGACTCAACTGG 1020  
 QY 1208 ACGCTTCCCGGTGACGCGGATTAACACGCGCCAGGTGGTGAATCTGTGTTGAACGCTGG 1267  
 Db 1021 ACGCTTCCCGGTGACGCGGATTAACACGCGCCAGGTGGTGAATCTGTGTTGAACGCTGG 1080  
 QY 1268 CGTGGGCTTAAGGATTAACAGCAGTGAATTCAGTTGGCTGGTCTTCTTCAAGCTTAAAG 1327  
 Db 1081 CGTGGGCTTAAGGATTAACAGCAGTGAATTCAGTTGGCTGGTCTTCTTCAAGCTTAAAG 1140  
 QY 1328 CAGATGCGGTATTAACAGCAGTGAATTCAGTTGGCTGGTCTTCTTCAAGCTTAAAG 1387  
 Db 1141 CAGATGCGGTATTAACAGCAGTGAATTCAGTTGGCTGGTCTTCTTCAAGCTTAAAG 1200  
 QY 1388 CTGGGAGGATGTAAGAGGGAATGCGAGGGGAGTGTGGTGGGAGGTTTAAAGCAA 1447  
 Db 1201 CTGGGAGGATGTAAGAGGGAATGCGAGGGGAGTGTGGTGGGAGGTTTAAAGCAA 1260  
 QY 1448 ATCGTGAATGAAGACGACATACCGGCTGTCAGTTGGTAAAT 1487  
 Db 1261 ATCGTGAATGAAGACGACATACCGGCTGTCAGTTGGTAAAT 1300

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RESULT 13
US-10-430-356-1
; Sequence 1, Application US/10430356
; Publication No. US20030232041A1
; GENERAL INFORMATION:
; APPLICANT: Kretz, Keith
; TITLE OF INVENTION: NOVEL PHYLASE
; FILE REFERENCE: 09010/029003
; CURRENT APPLICATION NUMBER: US/10/430,356
; PRIOR FILING DATE: 2003-05-05
; PRIOR APPLICATION NUMBER: US/09/580,515
; PRIOR FILING DATE: 1999-05-25
; PRIOR APPLICATION NUMBER: 09/318,528
; PRIOR FILING DATE: 1999-05-25
; PRIOR APPLICATION NUMBER: 09/291,931
; PRIOR FILING DATE: 1999-04-13
; PRIOR APPLICATION NUMBER: 08/910,798
; PRIOR FILING DATE: 1997-08-13
; PRIOR APPLICATION NUMBER: 09/259,214
; PRIOR FILING DATE: 1999-03-01
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1323
; TYPE: DNA
; ORGANISM: Escherichia coli
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1320)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(1323)
; OTHER INFORMATION: n = A,T,C or G
US-10-430-356-1

Query Match      67.7% Score 1287.8; DB 16; Length 1323;
Best Local Similarity 99.5% Pred. No. 0;
Matches 1293; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 188 ATGAAGGATCTTAATCCATTTTATCTCTGATCCGTTAACCCGCAATGCA 247
DB 1 ATGAAGGATCTTAATCCATTTTATCTCTGATCCGTTAACCCGCAATGCA 60
QY 248 TTCCTCAGAGTGAAGCCGAGCTGAAGTGAAGTGTGATGTCATGTCATGTC 307
DB 61 TTCCTCAGAGTGAAGCCGAGCTGAAGTGAAGTGTGATGTCATGTCATGTC 120
QY 308 GTGCGTGCTCAACCAAGGAGCCAGCACTGATGAGAGTGCACCCGAGAGCATGCGCA 367
DB 121 GTGCGTGCTCAACCAAGGAGCCAGCACTGATGAGAGTGCACCCGAGAGCATGCGCA 180
QY 368 ACTGAGCGGTAATAAATGAGTGTGCTGACACCGCGAGTGTGATGTCATGTCATGTC 427
DB 181 ACTGAGCGGTAATAAATGAGTGTGCTGACACCGCGAGTGTGATGTCATGTCATGTC 240
QY 428 GGAACATTAACAAGCGAGCGTCTGTGAGCGAGCGAATGTCGTGGGAAAGAGGCTGCGCG 487
DB 241 GGAACATTAACAAGCGAGCGTCTGTGAGCGAGCGAATGTCGTGGGAAAGAGGCTGCGCG 300
QY 488 CAGTCTGAGTGAAGTGCAGATTAATGCTGATGTGACAGAGCGTACCCGTAATAACAGCGAA 547
DB 301 CAGTCTGAGTGAAGTGCAGATTAATGCTGATGTGACAGAGCGTACCCGTAATAACAGCGAA 360
QY 548 GCGTTCGCGCGCGGCTGCGAGCTGACCTGATGCAATTAACCGACATTAACCCAGCGAGATAG 607
DB 361 GCGTTCGCGCGCGGCTGCGAGCTGACCTGATGCAATTAACCGACATTAACCCAGCGAGATAG 420
QY 608 TCCAGTCCCGATCCGTTATTTATCTCTTAATAAACTGGCGTTTGCACATGATTAACGCG 667
DB 421 TCCAGTCCCGATCCGTTATTTATCTCTTAATAAACTGGCGTTTGCACATGATTAACGCG 480

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QY 668 AACGTCAGAGCGATCCTCAGAGGAGGAGGAGTCAATGCTGACTTAAACGGGCAAT 727
DB 481 AACGTCAGAGCGATCCTCAGAGGAGGAGGAGTCAATGCTGACTTAAACGGGCAAT 540
QY 728 CGGCAAAACGGGCTTTCGGGAATCGGAACGGGCTGTTAATTTTCGGCAATCAACTGTGC 787
DB 541 CGGCAAAACGGGCTTTCGGGAATCGGAACGGGCTGTTAATTTTCGGCAATCAACTGTGC 600
QY 788 CTTAAACGTGAAGAAACAGGAGAAAGCTGTTAATTAACGAGGAGTAAACATCGGAATC 847
DB 601 CTTAAACGTGAAGAAACAGGAGAAAGCTGTTAATTAACGAGGAGTAAACATCGGAATC 660
QY 848 AAGGTAGCGCGCAATATGTCATTAACCGGTGCGTAAGCCTCGAATCAATGCTGACG 907
DB 661 AAGGTAGCGCGCAATATGTCATTAACCGGTGCGTAAGCCTCGAATCAATGCTGACG 720
QY 908 GAGATATTTTCTTCGCAACAGCAAGGAAATGCCAGAGCCGGGCTGGGAAAGATCAAC 967
DB 721 GAGATATTTTCTTCGCAACAGCAAGGAAATGCCAGAGCCGGGCTGGGAAAGATCAAC 780
QY 968 GATTCACACAGTGAACACCTTGCTAGTTGATTAACGCGCAATTTATTTCTACAA 1027
DB 781 GATTCACACAGTGAACACCTTGCTAGTTGATTAACGCGCAATTTATTTCTACAA 840
QY 1028 CGCAGCGCAAGAGTTGCCCGAGCCCGCAACCCGTTATTAATTAATGATCAACAGCG 1087
DB 841 CGCAGCGCAAGAGTTGCCCGAGCCCGCAACCCGTTATTAATTAATGATCAACAGCG 900
QY 1088 TTGACGCCCATCAACCGCAAAACAGGCGTATGATGATTAACCATTCAGTGTG 1147
DB 901 TTGACGCCCATCAACCGCAAAACAGGCGTATGATGATTAACCATTCAGTGTG 960
QY 1148 TTTATGCGCGGACAGCATTAATCTGCAAAATCTGCGCGCGCACTGAGCTCACTGCG 1207
DB 961 TTTATGCGCGGACAGCATTAATCTGCAAAATCTGCGCGCGCACTGAGCTCACTGCG 1020
QY 1208 ACGCTTCCCGGTCAAGCCGGAATPACAGCGCGAGGTGATGATGATGATGATGATGATGAT 1267
DB 1021 ACGCTTCCCGGTCAAGCCGGAATPACAGCGCGAGGTGATGATGATGATGATGATGATGAT 1080
QY 1268 CGTGGCTTAAGGATTAACAGCCAGTGAATTCAGGTTTCTGCTTTCAGACTTTACG 1327
DB 1081 CGTGGCTTAAGGATTAACAGCCAGTGAATTCAGGTTTCTGCTTTCAGACTTTACG 1140
QY 1328 CAGATGCGGATTAACAGCCGCTGCTATTAATACCGCGCGAGGAGTGAATACTGACC 1387
DB 1141 CAGATGCGGATTAACAGCCGCTGCTATTAATACCGCGCGAGGAGTGAATACTGACC 1200
QY 1388 CTGGCAGATGTGAAGAGGAAATGCGAGGAGCATGTGTGTTGGCAGGTTTACGCA 1447
DB 1201 CTGGCAGATGTGAAGAGGAAATGCGAGGAGCATGTGTGTTGGCAGGTTTACGCA 1260
QY 1448 ATCTGAATGAAGCAGCATTAACGGCGCTGCAATTTGTAAT 1487
DB 1261 ATCTGAATGAAGCAGCATTAACGGCGCTGCAATTTGTAAT 1300

RESULT 14
US-10-156-660-1
; Sequence 1, Application US/10156660
; Publication No. US20030103958A1
; GENERAL INFORMATION:
; APPLICANT: Short, Jay M.
; APPLICANT: Kretz, Keith
; APPLICANT: Gray, Kevin A.
; APPLICANT: Barton, Nelson R.
; APPLICANT: Garrett, James B.
; APPLICANT: O'Donoghue, Eileen
; TITLE OF INVENTION: PHYLASES, NUCLEIC ACIDS ENCODING THEM
; FILE REFERENCE: 09010-029007
; CURRENT APPLICATION NUMBER: US/10/156,660

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CURRENT FILING DATE: 2002-10-01  
 PRIOR APPLICATION NUMBER: US 09/866,379  
 PRIOR FILING DATE: 2001-05-24  
 PRIOR APPLICATION NUMBER: US 09/580,515  
 PRIOR FILING DATE: 2000-05-25  
 PRIOR APPLICATION NUMBER: US 09/318,528  
 PRIOR FILING DATE: 1999-05-25  
 PRIOR APPLICATION NUMBER: US 09/291,931  
 PRIOR FILING DATE: 1999-04-13  
 PRIOR APPLICATION NUMBER: US 09/259,214  
 PRIOR FILING DATE: 1999-03-01  
 PRIOR APPLICATION NUMBER: US 08/910,798  
 PRIOR FILING DATE: 1997-08-13  
 NUMBER OF SEQ ID NOS: 4  
 SOFTWARE: FastSeq for Windows Version 4.0  
 SEQ ID NO 1  
 LENGTH: 1308  
 TYPE: DNA  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: modified phytase enzyme.  
 NAME/KEY: CDS  
 LOCATION: (1)...(1308)  
 US-10-156-660-1

Query Match 66.5%; Score 1263.8; DB 15; Length 1308;  
 Best Local Similarity 98.2%; Pred. No. 0;  
 Matches 1277; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

188 ATGAAGGAGCTTATATCCATTTTATCTTCCTGATTCGTTAACCCGCAATTCGA 247  
 1 ATGAAGGAGCTTATATCCATTTTATCTTCCTGATTCGTTAACCCGCAATTCGA 60  
 248 TTCGCTCAGAGTGAAGCTGAAAGTGTGATGTGATGTGATGTGATGTGATGTGAT 307  
 61 TTCGCTCAGAGTGAAGCTGAAAGTGTGATGTGATGTGATGTGATGTGATGTGATGTGAT 120  
 308 GTGCTGTCTCCAAACCAAGGCCACGCACTGATGACAGATGTGATGATGATGATGATGATGAT 367  
 121 GTGCTGTCTCCAAACCAAGGCCACGCACTGATGACAGATGTGATGATGATGATGATGATGAT 180  
 368 ACCTGGCCGCTTAACTGGGTTGCTGACACCGCGAGTGTGATGATGATGATGATGATGATGAT 427  
 181 ACCTGGCCGCTTAACTGGGTTGCTGACACCGCGAGTGTGATGATGATGATGATGATGATGAT 240  
 428 GACATTTACCAACGCGAGGCTGTGATGACCGAGATGCTGGCGAAGGAGGCTGCCG 487  
 241 GACATTTACGCGAGGCTGTGATGACCGAGATGCTGGCGAAGGAGGCTGCCG 300  
 488 CAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 547  
 301 CAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 360  
 548 GCTTGTGCGCGCGGCTGCGCACTGATGTCATTAACCGTACATACCAGCGAGATACG 607  
 361 GCTTGTGCGCGCGGCTGCGCACTGATGTCATTAACCGTACATACCAGCGAGATACG 420  
 608 TCCATCCCGATCCGTTATTTATCTCTTAAATAATGGCGTTTGGCACTGGATTAACGCG 667  
 421 TCCATCCCGATCCGTTATTTATCTCTTAAATAATGGCGTTTGGCACTGGATTAACGCG 480  
 668 AACGTGACTGACCGATCTCTGACGAGGCGACAGAGGATCAATGCTGACTTTACCGGGCAT 727  
 481 AACGTGACTGACCGATCTCTGACGAGGCGACAGAGGATCAATGCTGACTTTACCGGGCAT 540  
 728 CGGCAAAACGCGCTTTTCCGCAACTGGAACGGGCTTATTTTCCGCAATCAACTGGCG 787  
 541 TATCAAAACGCGCTTTTCCGCAACTGGAACGGGCTTATTTTCCGCAATCAACTGGCG 600  
 788 CTTAAACGTAAGAAACAGAACGAAAGCTGTTCATTAAAGCAGGATTAACATCGGAATCTC 847  
 601 CTTAAACGTAAGAAACAGAACGAAAGCTGTTCATTAAAGCAGGATTAACATCGGAATCTC 660

848 AAGTGAAGCGCCGACATGCTCATTAACCGGATGCGTGAACCTCGCATCAATGCTGACG 907  
 661 AAGTGAAGCGCCGACATGCTCATTAACCGGATGCGTGAACCTCGCATCAATGCTGACG 720  
 908 GAGATTTTCTCTCTGCAACAGCAAGGAAATGCGGAGCCGGGTGGGAAAGATTCACC 967  
 721 GAGATTTTCTCTCTGCAACAGCAAGGAAATGCGGAGCCGGGTGGGAAAGATTCACC 780  
 968 GATTACACCAAGTGAACACTTGTCTAAGTTGATTAAGCGCATTTTATTTGCTACAA 1027  
 781 GATTACACCAAGTGAACACTTGTCTAAGTTGATTAAGCGCATTTTATTTGCTACAA 840  
 1028 CGCAGCGCAGAGGTTGCGCGCAGCGCGCCACCCGTTATTAAGTTGATTAAGCGCAT 1087  
 841 CGCAGCGCAGAGGTTGCGCGCAGCGCGCCACCCGTTATTAAGTTGATTAAGCGCAT 900  
 1088 TTGAGCGCCCATCCACCGCAAAACAGGCGTATGATGATGATGATGATGATGATGATGATGAT 1147  
 901 TTGAGCGCCCATCCACCGCAAAACAGGCGTATGATGATGATGATGATGATGATGATGATGAT 960  
 1148 TTATGCGCGACACGATTAATCTGCAATCTGCGCGCGCACTGAGCTCAACTGG 1207  
 961 TTATGCGCGACACGATTAATCTGCAATCTGCGCGCGCACTGAGCTCAACTGG 1020  
 1208 AGCTTCCCGGTACGCGGATTAACAGCGCGCAAGTGTGATGATGATGATGATGATGATGATGAT 1267  
 1021 AGCTTCCCGGTACGCGGATTAACAGCGCGCAAGTGTGATGATGATGATGATGATGATGATGAT 1080  
 1268 CGTGGCTAAGCGATTAACAGCGCGCAAGTGTGATGATGATGATGATGATGATGATGATGATGAT 1327  
 1081 CGTGGCTAAGCGATTAACAGCGCGCAAGTGTGATGATGATGATGATGATGATGATGATGATGAT 1140  
 1328 CAGATCGGTATTAACCGCGCTGTCTATTAATAGCGCGCGGAGAGTGAACCTGACC 1387  
 1141 CAGATCGGTATTAACCGCGCTGTCTATTAATAGCGCGCGGAGAGTGAACCTGACC 1200  
 1388 CTGGCAGATGATGAAGAGGAATGCGCAGGCGATGTTCTGTTGGCAGTTTACGCA 1447  
 1201 CTGGCAGATGATGAAGAGGAATGCGCAGGCGATGTTCTGTTGGCAGTTTACGCA 1260  
 1448 ATCGTAATGAAGACGACATACCGCGGTGACGTTGTAAT 1487  
 1261 ATCGTAATGAAGACGACATACCGCGGTGACGTTGTAAT 1300

# RESULT 15

US-10-334-672-4  
 Sequence 4, Application US/10334672  
 Publication No. US20030157646A1  
 GENERAL INFORMATION:  
 APPLICANT: Lananan, Mike  
 APPLICANT: Koepf, Edward  
 TITLE OF INVENTION: Microbially-Expressed Thermotolerant Phytase For Animal Feed  
 FILE REFERENCE: SYNG-P01-001  
 CURRENT APPLICATION NUMBER: US/10/334,672  
 PRIOR APPLICATION NUMBER: 60/344,523  
 PRIOR FILING DATE: 2001-12-28  
 NUMBER OF SEQ ID NOS: 4  
 SOFTWARE: PatentIn version 3.1  
 SEQ ID NO 4  
 LENGTH: 1281  
 TYPE: DNA  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: No. US20030157646A19X gene  
 US-10-334-672-4

Query Match 35.2%; Score 669.6; DB 15; Length 1281;  
 Best Local Similarity 71.3%; Pred. No. 1;le-220;  
 Matches 882; Conservative 0; Mismatches 355; Indels 0; Gaps 0;

Tue May 4 07:05:30 2004

us-09-866-379d-7.rnpb

Page 16

QY 251 GCTCAGATGAGCCGAGCTGAAAGCTGAAAAGTGTGATTTGTCACTGCTCAATGCTGTG 310  
Db 28 GCTCAATCTGAAACGAGATGAAAGTGGAAATCTGTGTCAATGCTTCCCAACACGAGTGT 87  
QY 311 CGTCTCCCAACCAAGGCGACGCACTGATGAGGATGTCAACCCCAAGACGATGAGCCAAAC 370  
Db 88 AGAGCTCCAACTAAAGGCTACTCACTGATGCAAGATGTCTCAAGATGCTGAGCTTACC 147  
QY 371 TGGCCGCTAAATCTGGGTGCTGACACCGCGAGTGTGAGCTAATGCTTATCTGGA 430  
Db 148 TGGCTGTAAAGTGGGTGAATGATCTCAAGAGTGTGATGATGATGCTTACTTGGGT 207  
QY 431 CATTAACCAACCCGACGCTGTGTGAGCCGACGATTTGCTGCGAATAAGGCTGCCGAG 490  
Db 208 CACTACTGAGACAAAGATGT 267  
QY 491 TCTGTGAGTGTGCGATTAATGCTGATGTCAGACGAGCTACCCGTAATAACAGGCGAGCC 550  
Db 268 TCTGTGAGTGTGCTATCATTTGCTGATGTTGATGAAAGACTAGAAAGCTGAGGAGCC 327  
QY 551 TTGCGCCGCGGCTGCGACCTGACTGTGCAATACCGTACATACCAGGAGATAGCTCC 610  
Db 328 TTGCTGTGCGGTTGTGCGCCGAGCTGTGCTATCACTGTTCACACTCAAGCTGATCTTC 387  
QY 611 AGTCCCGATCGGTTAATTAATCTCTTAATAAAGCTGCTTGCCTCACTGATTAACGCGAAC 670  
Db 388 TCTCCAGATCATTTGCTCAACCTCATGAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 447  
QY 671 GTGACTGACGCTGCTGACGAGGCGAGAGGCTCAATGTGTGCTTACCGGCGATCGG 730  
Db 448 GTTACTGTGCTGCTGTGAGAAAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 507  
QY 731 CAACCGGCTTGTGCGAACTGAAACGAGGCTGTATTTTCCGCAATCAAACTTGTGCTT 790  
Db 508 CAATCTGCTTCAAGATTTGAAAGATCTTGAACCTTCCCAATCTTAACTGTGTGTGT 567  
QY 791 AAACGTGAAACAGAGCAAGAAAGCTTCAATTAACGAGGCTTACCATCGAACTCAAG 850  
Db 568 AAGAGAGAGAGCAAGAGATCTTGTCTTGTGCTCAAGCTTCCATCTGAATGAAAG 627  
QY 851 GTGAGCGCGCGCAATGTCTCAATTAACGAGGCTGAGCTTCAATGTGAGCGAG 910  
Db 628 GTCTGTGTGATGT 687  
QY 911 ATATTTCTCTGCAACAGCAACAGGAATGCGGAGCCGAGGCTGAGGAAGATCAAGAT 970  
Db 688 ATCTTCTGTGCAACAGCTCAAGGTATGCCAGAACAGGCTGAGGATGATCATGAT 747  
QY 971 TCACACGAGTGAACCTTGTGTAAGTGTGATAACGCGCAATTTTATTTGTCTCAACGC 1030  
Db 748 TCTCACATGAGAACCTTGT 807  
QY 1031 ACGCCAGAGTGTGCGGAGCGCGCACCCGCTTATTAATTTGATCAAGACAGCGTTG 1090  
Db 808 ACTCCAGAGTGTGCTAAGTATCCAGAGCTACTCATTTGTGATGATCAAGACAGCGTTG 867  
QY 1091 ACGCCCATCCACCGGCAAAAACGAGCGATGTGTGATTAACCATTCAGTGTGTGT 1150  
Db 868 ACTCCACACCAACAGAGAGAGCTTACGTTACCTTGCACACTTGTGTGTGTGTGTGTGT 927  
QY 1151 ATGCGCGAGCAAGATTAATCTGCAAAATCTGCGCGGCGCATGAGCTCACTGAGAG 1210  
Db 928 ATTGCGGCTGACGATTAATTAATCTGCTAATCTTGTGTGTGTGTGTGTGTGTGTGTGT 987  
QY 1211 CTTCCCGGCTGACCGGATTAACGCGCGGAGTGTGATGATGATGATGATGATGATGATG 1270  
Db 988 TTGCGAGGCTGACGAGATTAACCTCAACAGGCTGTGATGATGATGATGATGATGATGATG 1047  
QY 1271 CGGCTAAGGATTAACGAGCTGATGATGATGATGATGATGATGATGATGATGATGATG 1330  
Db 1048 CGACTGTGTGATTAATCTCAATGATTAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1107

QY 1331 ATGCGGATTAACGCGGCTGTGATTAATACGCGCGCGGAGAGTGAATGACCTTG 1390  
Db 1108 ATGAGAGCAAGACTCCATTTGTCTTGAACCTCAACAGGTGAAGTCAAGTTGACCTTG 1167  
QY 1391 GCAAGATGTGAAGACGAAATGCGAGGCGATGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1450  
Db 1168 GCTGTGTGAAGAAAGAACGCTCAAGGTATGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1227  
QY 1451 GTGAATGAAGACGAGATACCGGCGTGTGAGTTGTAT 1487  
Db 1228 GTCAAGAGGCGAGATCCAGCTTGTCTTGTAT 1264

Search completed: May 2, 2004, 00:50:59  
Job time : 778.893 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 1, 2004, 21:37:37 / Search time 151.653 Seconds  
(without alignments)  
6956.396 Million cell updates/sec

Title: US-09-866-379D-7  
Perfect score: 1901  
Sequence: 1 taagagacagaacaacatg.....gtaatgacgacgcgacg 1901

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents NA.\*  
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2: /cgm2\_6/ptodata/2/ina/5B.COMB.seq.\*  
3: /cgm2\_6/ptodata/2/ina/6A.COMB.seq.\*  
4: /cgm2\_6/ptodata/2/ina/6B.COMB.seq.\*  
5: /cgm2\_6/ptodata/2/ina/PTCUS.COMB.seq.\*  
6: /cgm2\_6/ptodata/2/ina/backfile1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1397.4	73.5	1489	US-09-540-149A-9	Sequence 9, Appl1
2	1287.8	67.7	1323	US-09-259-214-1	Sequence 1, Appl1
3	1287.8	67.7	1323	US-09-318-528-1	Sequence 1, Appl1
4	1287.8	67.7	1323	US-09-291-931-1	Sequence 1, Appl1
5	1175.8	61.9	1272	US-08-910-798-1	Sequence 1, Appl1
6	120.2	6.3	2226	US-09-488-039A-440	Sequence 940, App
7	73.2	3.9	2202	US-09-328-352-1473	Sequence 1473, App
8	63.6	3.3	1266	US-09-489-039A-341	Sequence 341, App
9	55.2	2.9	2337	US-09-934-899-7	Sequence 7, Appl1
10	51.4	2.7	5738	US-08-956-171E-84	Sequence 84, Appl1
11	41.8	2.2	2326	US-09-634-238-28	Sequence 28, Appl1
12	39.8	2.1	2868	US-09-710-794-4	Sequence 4, Appl1
13	38.4	2.0	1664976	US-08-916-421B-1	Sequence 1, Appl1
14	37.2	2.0	1053	US-09-252-991A-11337	Sequence 11337, A
15	37.2	2.0	2334	US-09-254-991A-11253	Sequence 11253, A
16	37.2	2.0	6545	PCT-US95-13749-3	Sequence 3, Appl1
17	36.4	1.9	7480	US-09-252-991A-15917	Sequence 15917, A
18	36.4	1.9	7480	US-09-252-991A-15888	Sequence 15888, A
19	36.4	1.9	885	US-09-252-991A-15774	Sequence 15774, A
20	36.4	1.9	1068	US-09-252-991A-15804	Sequence 15804, A
21	35.8	1.9	505	US-09-621-976-15639	Sequence 15639, A
22	35.2	1.9	900	US-09-252-991A-2887	Sequence 2887, Ap
23	35.2	1.9	1035	US-09-252-991A-28702	Sequence 2702, Ap
24	35.2	1.9	6545	PCT-US95-13749-3	Sequence 3, Appl1
25	35.2	1.9	7218	US-08-232-463-14	Sequence 14, Appl1
26	34.4	1.8	93	US-09-453-702B-24	Sequence 24, Appl1
27	34.4	1.8	3076	US-09-710-794-1	Sequence 1, Appl1

C 28	34.4	1.8	3376	4	US-09-620-312D-116	Sequence 116, App
C 29	34.4	1.8	3442	4	US-09-620-312D-115	Sequence 115, App
C 30	34.4	1.8	4403765	3	US-09-103-840A-2	Sequence 2, Appl1
C 31	34.4	1.8	4411529	3	US-09-103-840A-1	Sequence 1, Appl1
C 32	34	1.8	998	2	US-07-885-089B-5	Sequence 5, Appl1
C 33	34	1.8	1044	4	US-09-252-991A-8907	Sequence 8907, Ap
C 34	34	1.8	1068	4	US-09-710-794-3	Sequence 8656, Ap
C 35	34	1.8	2313	4	US-09-252-991A-8696	Sequence 9082, Ap
C 36	34	1.8	2706	4	US-09-252-991A-9082	Sequence 1, Appl1
C 37	33.6	1.8	1843	1	US-07-918-023-1	Sequence 8976, Ap
C 38	33.4	1.8	399	4	US-09-441-340-1	Sequence 21, Appl1
C 39	33.4	1.8	15611	4	US-08-387-942C-21	Sequence 497, App
C 40	33.2	1.7	1155	2	US-08-765-907A-9	Sequence 6, Appl1
C 41	33.2	1.7	1194	4	US-08-765-907A-9	Sequence 1, Appl1
C 42	33.2	1.7	1584	4	US-09-489-039A-497	Sequence 993, App
C 43	33.2	1.7	4496	2	US-08-765-907A-6	
C 44	33.2	1.7	12588	2	US-08-387-942C-1	
C 45	33	1.7	357	4	US-09-620-312D-993	

## ALIGNMENTS

RESULT 1  
US-09-540-149A-9  
Sequence 9, Application US/09540149A  
Patent No. 6511699  
GENERAL INFORMATION:  
APPLICANT: Lei, Xing  
TITLE OF INVENTION: ENZYMES WITH IMPROVED PHYTASE ACTIVITY  
FILE REFERENCE: 19603/2791  
CURRENT APPLICATION NUMBER: US/09/540,149A  
PRIOR FILING DATE: 2000-03-31  
PRIOR APPLICATION NUMBER: 60/127,032  
NUMBER OF SEQ ID NOS: 9  
SOFTWARE: Patentin Ver. 2.1  
SEQ ID NO 9  
LENGTH: 1489  
? ORGANISM: Escherichia coli  
? US-09-540-149A-9

Query Match 73.5%; Score 1397.4; DB 4; Length 1489;  
Best Local Similarity 97.1%; Pred. No. 0;  
Matches 1445; Conservative 0; Mismatches 37; Indels 6; Gaps 2;

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QY	61	CTCTCACCCCTGTGTGTAATGCTGACCCGCGCTGAAAGTTAAGAGCTAGGCC	120
DB	61	CTCTCACCCCTGTGTGTAATGCTGACCCGCGCATTTTGTGATGTTGCG	120
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DB	121	TGATGCGGCGCATTAACATGCAATCAATATGCAATATGCAATATGCAATATG	180
QY	181	CAATGAGAAAGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCA	240
DB	181	CAATGAGAAAGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCA	240
QY	241	ATCTGATTCGCTCAAGATGAGCGGAGCTGAAGCTGAAGCTGAAGCTGAAGCTG	300
DB	241	ATCTGATTCGCTCAAGATGAGCGGAGCTGAAGCTGAAGCTGAAGCTGAAGCTG	300
QY	301	TGATGCTGCGCTGCTCAAGATGAGCGGAGCTGAAGCTGAAGCTGAAGCTGAAG	360
DB	301	TGATGCTGCGCTGCTCAAGATGAGCGGAGCTGAAGCTGAAGCTGAAGCTGAAG	360
QY	361	ATGAGCACTGCGCGCTGAAGCTGATGATGATGATGATGATGATGATGATGATG	420
DB	361	ATGAGCACTGCGCGCTGAAGCTGATGATGATGATGATGATGATGATGATGATG	420



355 ATGCGCAACTGGCGGTAATACTGGGTTGGCTGACACACGCGGTGAGCTAATCGC 414  
421 CTATCTCGGAGATTACCAACGCGCAGCGCTCTGGTAGCCGAGGATTTGTCGCGAAAAAGG 480  
415 CTATCTCGGAGATTACCAACGCGCAGCGCTCTGGTAGCCGAGGATTTGTCGCGAAAAAGG 474  
481 CTGCCCCGAGTCTGCTGAGGTCGCGATTATTTGCTGATGTCGACGAGCTACCCGTAAC 540  
475 CTGCCCCGAGTCTGCTGAGGTCGCGATTATTTGCTGATGTCGACGAGCTACCCGTAAC 534  
541 AGCGCAAGCTCTGCGCGCGCGGCTGCGACCTGACTGTCAATTAACCGTACACCGAGC 600  
535 AGCGCAAGCTCTGCGCGCGCGGCTGCGACCTGACTGTCAATTAACCGTACACCGAGC 594  
601 AGATACGTCCAGTCCCGATCCGTTATTTATCTCTTAAAACTGGCGTTTGCACATGGA 660  
595 AGATACGTCCAGTCCCGATCCGTTATTTATCTCTTAAAACTGGCGTTTGCACATGGA 654  
661 TAACGCGAAGCTGAGTGAAGGATCTGACGAGGCGAGAGGTCATTTGCTGACTTAC 720  
655 TAACGCGAAGCTGAGTGAAGGATCTGACGAGGCGAGAGGTCATTTGCTGACTTAC 714  
721 CGGCGATCGGCAAAAGCGCGTTTCGGAACGAGGTCGTTAATTTCCGCAATCAA 780  
715 CGGCGATCGGCAAAAGCGCGTTTCGGAACGAGGTCGTTAATTTCCGCAATCAA 774  
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775 CTGTCGCTTAAAGTGAAGGATCTGACGAGGTCATTTGCTGACTTAC 834  
841 GGAATCAAGGTGAGCGCGCGCAATGTCATTAACCGGTCGCTGAAAGCTCGCATCAAT 900  
835 GGAATCAAGGTGAGCGCGCGCAATGTCATTAACCGGTCGCTGAAAGCTCGCATCAAT 894  
901 GCTGACGAGATATTTCTCTGCAACAAGCAAGGAAATGCCGAGCCGCGGTGGAGAG 960  
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961 GATCAACCATTCACACAGTGAAGCACTTGTAAATTGATTAACGCGCAATTTTATTT 1020  
955 GATCAACCATTCACACAGTGAAGCACTTGTAAATTGATTAACGCGCAATTTTATTT 1014  
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1195 CAATGACAGCTTCCCGGTGACGCGGATTAACAGCGCGCGCAGAGTGTGAGTGTGTA 1254  
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1255 AGCGTGGCGTGGCTAAGCGATTAACAGCGCGATTAAGGTTTTCGCTGCTTTCAGAC 1314  
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1315 TTTCAGAGAGATGCGTGAATAAAGCGCGCTGATTAATTAAGCGCGCGCGAGAGTGA 1374  
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1375 ACTGACCTTGGAGAGATGTAAGAGCGAATGCGAGGCGATGTTGTTGCGAGGTTT 1434  
1441 TACGCAATCGTGAATGAAGACGATACCGCGCGTGAATTTGTAAG 1488  
1435 TACGCAATCGTGAATGAAGACGATACCGCGCGTGAATTTGTAAG 1482

RESULT 2  
US-09-259-214-1  
; Sequence 1, Application US/09259214A  
; Patent No. 6110719  
; GENERAL INFORMATION:  
; APPLICANT: Kretz, Keith  
; TITLE OF INVENTION: NOVEL PHYTASE  
; FILE REFERENCE: DIVER1370-1  
; CURRENT APPLICATION NUMBER: US/09/259,214A  
; EARLIER FILING DATE: 1999-03-01  
; EARLIER APPLICATION NUMBER: 08/910,798  
; EARLIER FILING DATE: 1997-08-13  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 1323  
; TYPE: DNA  
; ORGANISM: Escherichia coli  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)...(1320)  
; NAME/KEY: misc feature  
; LOCATION: (1)...(1323)  
; OTHER INFORMATION: n = A,T,C or G  
US-09-259-214-1  
Query Match 67.7%; Score 1287.8; DB 3; Length 1323;  
Best Local Similarity 99.5%; Pred. No. 0;  
Matches 1233; Conservative 0; Mismatches 7; Indels 0; Gaps 0;  
QY 188 ATCAAAGCATCTTAATCCCATTTTATCTTCTGATTCCTGTAACCCCGAATCTGCA 247  
DB 1 ATCAAAGCATCTTAATCCCATTTTATCTTCTGATTCCTGTAACCCCGAATCTGCA 60  
QY 248 TTGCTCAGAGTGAAGCGGAGCTGAAGCTGAAGTGTGTGATTTGTCAGTGTGATGAT 307  
DB TTGCTCAGAGTGAAGCGGAGCTGAAGCTGAAGTGTGTGATTTGTCAGTGTGATGAT 120  
QY 308 GTGCGTCTTCAACCAAGCCACGCACTGATGCAAGATGTCAACCCGAGCGATGGCA 367  
DB GTGCGTCTTCAACCAAGCCACGCACTGATGCAAGATGTCAACCCGAGCGATGGCA 180  
QY 121 GTGCGTCTTCAACCAAGCCACGCACTGATGCAAGATGTCAACCCGAGCGATGGCA 180  
DB ACCTGCGCGGTAAAACTGGGTTGGCTGACACCGCGAGTGTGATGCTATGCTC 427  
QY 368 ACCTGCGCGGTAAAACTGGGTTGGCTGACACCGCGAGTGTGATGCTATGCTC 427  
DB ACCTGCGCGGTAAAACTGGGTTGGCTGACACCGCGAGTGTGATGCTATGCTC 240  
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DB GGAATTAACCAAGCCAGCTGCTGTAAGCGGATTTGTCGCAAAAAGGCTGCCG 300  
QY 241 GGAATTAACCAAGCCAGCTGCTGTAAGCGGATTTGTCGCAAAAAGGCTGCCG 300  
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DB CAGTGTGTCAGGTGCGATTAATGCTGATGTCGACGAGCGTAAACCGTAACAGCGCA 360  
QY 301 CAGTGTGTCAGGTGCGATTAATGCTGATGTCGACGAGCGTAAACCGTAACAGCGCA 360  
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QY 608 TTCAGTCCCGATCCGTTATTTAATCCTTAATAAATGCGGTTTGGCACTGTAACGCG 667  
DB TTCAGTCCCGATCCGTTATTTAATCCTTAATAAATGCGGTTTGGCACTGTAACGCG 480  
QY 421 TCCAGTCCCGATCCGTTATTTAATCCTTAATAAATGCGGTTTGGCACTGTAACGCG 480  
DB TCCAGTCCCGATCCGTTATTTAATCCTTAATAAATGCGGTTTGGCACTGTAACGCG 480  
QY 668 AACGTACTGACGCGATCTCTGACAGGCGAGAGGCTCAATTTGTAATTCGCGGAT 727  
DB AACGTACTGACGCGATCTCTGACAGGCGAGAGGCTCAATTTGTAATTCGCGGAT 540  
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Db      661 AAGGTGAGCCGCGCAATGTTCTATTAACCGGTGCGGTAAAGCTTCGATCAATGCTAGC 720
Qy      908 GAGATATTTCTCCGCAACAGGACAGGGAAATGCGAGCGGGGTGGGGAAGATACC 967
Db      721 GAGATATTTCTCCGCAACAGGACAGGGAAATGCGAGCGGGGTGGGGAAGATACC 780
Qy      968 GATTCAACACAGTGAACACCTTGTGAAGTTGCAATAACGGCAATTTATTTGCTACAA 1027
Db      781 GATTCAACACAGTGAACACCTTGTGAAGTTGCAATAACGGCAATTTATTTGCTACAA 840
Qy      1028 CGCAGCCGAGAGTTGCGCCGAGCGCGCACCCCGTTATTAAGTTGATCAACAGCAGC 1087
Db      841 CGCAGCCGAGAGTTGCGCCGAGCGCGCACCCCGTTATTAAGTTGATCAACAGCAGC 900
Qy      1088 TTGAAGCCCATCCACCGCAAAAACAGCGTATGATGATTAATTAATTAATTAATTAAT 1147
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Qy      1148 TTATTCGCGCGGACACGATCTAATCTGCGCAATCTCGCGCGCGCATGAGCTCAATCG 1207
Db      961 TTATTCGCGCGGACACGATCTAATCTGCGCAATCTCGCGCGCGCATGAGCTCAATCG 1020
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Qy      1268 CGTGGCGTAAAGCAATACAGCAGTGAATTCAGGTTTCGCTGCTTCGACACTTAACG 1327
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Qy      1328 CAGATGCGGTAAACAGCGCTGTCATTAATACGCGCGCGCGGAGAGTGAACGAGC 1387
Db      1141 CAGATGCGGTAAACAGCGCTGTCATTAATACGCGCGCGCGGAGAGTGAACGAGC 1200
Qy      1388 CTGGCAGAGTGTGAAGAGCGGAATGCGCAGGGCATGTGTTGTTGGCAGGTTTACGCA 1447
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RESULT 3
US-09-318-528-1
; Sequence 1, Application US/09318528
; Patent No. 6183740
; GENERAL INFORMATION:
; APPLICANT: Kretz, Keith
; TITLE OF INVENTION: NOVEL PHYTASE
; FILE REFERENCE: 09010/029003
; CURRENT APPLICATION NUMBER: US/09/318,528
; EARLIER FILING DATE: 1999-05-25
; EARLIER APPLICATION NUMBER: 09/291,931
; EARLIER FILING DATE: 1999-04-13
; EARLIER APPLICATION NUMBER: 08/910,798
; EARLIER FILING DATE: 1997-08-13
; EARLIER APPLICATION NUMBER: 09/259,214
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1323
; TYPE: DNA
; ORGANISM: Escherichia coli
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1320)

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; NAME/KEY: misc_feature
; LOCATION: (1)...(1323)
; OTHER INFORMATION: n = A,T,C or G
US-09-318-528-1

Query Match      67.7%; Score 1287.8; DB 3; Length 1323;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 1293; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy      188 ATGAAGGAGATTTAATCCCATTTTATCTCTTGATTCCTGTTAACCCCGCAATCTGCA 247
Db      1 ATGAAGGAGATTTAATCCCATTTTATCTCTTGATTCCTGTTAACCCCGCAATCTGCA 60
Qy      248 TTGCGCTCAGAGTGAAGCCGAGCTGAAGCTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 307
Db      61 TTGCGCTCAGAGTGAAGCCGAGCTGAAGCTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 120
Qy      308 GTGCGTCTCCAAACCAAGGCAACGCACTGATGAGATGTCATCCCAAGCAGCATGGCCA 367
Db      121 GTGCGTCTCCAAACCAAGGCAACGCACTGATGAGATGTCATCCCAAGCAGCATGGCCA 180
Qy      368 ACGTGGCCGCTAAACTGCTGTTGCTGACACCGCGAGGTGGTGAAGTGAAGTGAAGTGAAG 427
Db      181 ACGTGGCCGCTAAACTGCTGTTGCTGACACCGCGAGGTGGTGAAGTGAAGTGAAGTGAAG 240
Qy      428 GGCATTAACCAAGCAGCGTCTGTTAGCCGACGATTTGCTGGCCGAAAAGGGCTGCCG 487
Db      241 GGCATTAACCAAGCAGCGTCTGTTAGCCGACGATTTGCTGGCCGAAAAGGGCTGCCG 300
Qy      488 CAGTCTGCTCAGTGGCGATTTTGTGATGTCACAGCGTAAACCGTTAAACAGGCGCA 547
Db      301 CAGTCTGCTCAGTGGCGATTTTGTGATGTCACAGCGTAAACCGTTAAACAGGCGCA 360
Qy      548 GCGTTGCGCGCGGCTGGACCTGACTGTGCAATTAACGTAACATCCAGGAGATACG 607
Db      361 GCGTTGCGCGCGGCTGGACCTGACTGTGCAATTAACGTAACATCCAGGAGATACG 420
Qy      608 TCGAGTCCCGATCGGTTAATTTAATCTCTTAATAACCTGCGCTTGGCAACTGAGTAAACGCG 667
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Qy      668 AACGTGACAGAGCATCTCTGACAGGAGAGAGGTCAATTGCTTAACCGGAGAT 727
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Qy      728 CGGCAAAACGCGCTTTCGCAACTGGAACGGGTCTTAATTTTCGCAATCAAACTTGTGC 787
Db      541 CGGCAAAACGCGCTTTCGCAACTGGAACGGGTCTTAATTTTCGCAATCAAACTTGTGC 600
Qy      788 CTTAAACGTGAAGAACAGGAGGAAAGCTGTTAATTAAGCAGGAGTTTCAATCGGAATC 847
Db      601 CTTAAACGTGAAGAACAGGAGGAAAGCTGTTAATTAAGCAGGAGTTTCAATCGGAATC 660
Qy      848 AAGGTGAGCCGCGCAATGTTCTATTAACCGGTGCGGTAAAGCTTCGATCAATGCTAGC 907
Db      661 AAGGTGAGCCGCGCAATGTTCTATTAACCGGTGCGGTAAAGCTTCGATCAATGCTAGC 720
Qy      908 GAGATATTTCTCCGCAACAGGACAGGGAAATGCGAGCGGGGTGGGGAAGATACC 967
Db      721 GAGATATTTCTCCGCAACAGGACAGGGAAATGCGAGCGGGGTGGGGAAGATACC 780
Qy      968 GATTCAACACAGTGAACACCTTGTGAAGTTGCAATAACGGCAATTTATTTGCTACAA 1027
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Qy      1028 CGCAGCCGAGAGTTGCGCCGAGCGCGCACCCCGTTATTAAGTTGATCAACAGCAGC 1087
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Qy      1088 TTGAAGCCCATCCACCGCAAAAACAGCGTATGATGATTAATTAATTAATTAATTAAT 1147
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 Db 1201 CTGGCAGATGTAAGAGCGAAATCGCAGGCGATGTTGGTGGCAGGTTTAAAGCAA 1260  
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## RESULT 4

US-09-291-931-1

/ Sequence 1, Application US/09291931A

/ Patent No. 6130897

/ GENERAL INFORMATION:

/ APPLICANT: Kretz, Keith

/ TITLE OF INVENTION: NOVEL PHYTASE

/ FILE REFERENCE: 09010/029003

/ CURRENT APPLICATION NUMBER: US/09/291,931A

/ EARLIER FILING DATE: 1999-04-13

/ EARLIER APPLICATION NUMBER: 08/910,798

/ EARLIER FILING DATE: 1997-08-13

/ EARLIER APPLICATION NUMBER: 09/259,214

/ EARLIER FILING DATE: 1999-03-01

/ NUMBER OF SEQ ID NOS: 4

/ SOFTWARE: FastSeq for Windows Version 4.0

/ SEQ ID NO 1

/ LENGTH: 1323

/ TYPE: DNA

/ ORGANISM: Escherichia coli

/ FEATURE:

/ NAME/KEY: CDS

/ LOCATION: (1)...(1320)

/ NAME/KEY: misc. feature

/ LOCATION: (1)...(1323)

/ OTHER INFORMATION: n = A,T,C or G

US-09-291-931-1

Query Match 67.7%; Score 1287.8; DB 3; Length 1323;  
 Best Local Similarity 99.5%; Pred. No. 0;  
 Matches 1293; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 188 ATGAAGGATCTTAATCCATTTTATCTCTTCTGATTCCTGTTAAACCCCGCATCTGCA 247  
 Db 1 ATGAAGGATCTTAATCCATTTTATCTCTTCTGATTCCTGTTAAACCCCGCATCTGCA 60  
 QY 248 TTGCTCAGAGTGAACCGGAGCTGAAGCTGAAGTGTGTGATTTGTCAGTGCATAGT 307  
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 QY 308 GTGCGTGTCTCCAAACCAAGCCGCAAGTGAATGTCAGATCCCAAGAGCATGCGCA 367  
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 QY 368 ACGTGGCCGCTAAACCTGGTGTGCTGACACCGGAGGTGTGATGCTAATCGCTATCTC 427  
 Db 181 ACGTGGCCGCTAAACCTGGTGTGCTGACACCGGAGGTGTGATGCTAATCGCTATCTC 240

QY 428 GGAATTAACCAACGCAAGCTGTGTAGCCGACGATTTGCTGCGCAAAAAAGGCTGCCCC 487  
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 QY 488 CAGTCTGTCAAGTGGCGATTTATGCTGATGTGACGAGACGTAACCGCTAAACAGGCGAA 547  
 Db 301 CAGTCTGTCAAGTGGCGATTTATGCTGATGTGACGAGACGTAACCGCTAAACAGGCGAA 360  
 QY 548 GCGTTCGCGCGCGGCTGCGACCTGACCTGTGCAATTAACCGTACATACCAGGCAATAG 607  
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 QY 608 TCCAGTCCCGATCCCGTTATTTATCTCTTAATAAATCGGCGTTTGGCAATGATTAACGG 667  
 Db 421 TCCAGTCCCGATCCCGTTATTTATCTCTTAATAAATCGGCGTTTGGCAATGATTAACGG 480  
 QY 668 AACGTACTGACGCGATCTCTGACAGGCGAGAGGCTCAATTGCTGACTTTAACCGGCAAT 727  
 Db 481 AACGTACTGACGCGATCTCTGACAGGCGAGAGGCTCAATTGCTGACTTTAACCGGCAAT 540  
 QY 728 CCGCAACCGCGCTTTGCGCACTGGAACGGGTGCTTAATTTCCGCAATCAACTTTGCG 787  
 Db 541 CCGCAACCGCGCTTTGCGCACTGGAACGGGTGCTTAATTTCCGCAATCAACTTTGCG 600  
 QY 788 CTTAAACGTGAGAAACAGACAGCAAGCTGTCTATTACGACAGCATTAACATCGGAATCTC 847  
 Db 601 CTTAAACGTGAGAAACAGACAGCAAGCTGTCTATTACGACAGCATTAACATCGGAATCTC 660  
 QY 848 AAGGTAGCGCGCGCAATGCTCTCAATTAACCGGTGGGTAAAGCTTGCATCAATGCTGAC 907  
 Db 661 AAGGTAGCGCGCGCAATGCTCTCAATTAACCGGTGGGTAAAGCTTGCATCAATGCTGAC 720  
 QY 908 GAGATATTTCTCTCTGCAACAGCAAGGATGCGGAGCCGCGGTGGGAAAGATCAC 967  
 Db 721 GAGATATTTCTCTCTGCAACAGCAAGGATGCGGAGCCGCGGTGGGAAAGATCAC 780  
 QY 968 GATTCAACCAAGTGAACCACTTGTCTAATTGTCATTAACGCGCAATTTATTGCTACAA 1027  
 Db 781 GATTCAACCAAGTGAACCACTTGTCTAATTGTCATTAACGCGCAATTTATTGCTACAA 840  
 QY 1028 CGGAGCGCAAGGTTGCGCGGAGCGCGCGCAACCGGTTATTAATTGATGAAGAAGCG 1087  
 Db 841 CGGAGCGCAAGGTTGCGCGGAGCGCGCGCAACCGGTTATTAATTGATGAAGAAGCG 900  
 QY 1088 TTGACGCCCCATCTCACCGCAAAAACAGGCGTATGTGTGACATTAACCACTTCACTG 1147  
 Db 901 TTGACGCCCCATCTCACCGCAAAAACAGGCGTATGTGTGACATTAACCACTTCACTG 960  
 QY 1148 TTATATCGCCGACAGATATCTAATCTGGCAATCTCGCGCGGCACTGAGCTCAATCG 1207  
 Db 961 TTATATCGCCGACAGATATCTAATCTGGCAATCTCGCGCGGCACTGAGCTCAATCG 1020  
 QY 1208 ACGCTTCCCGGTCAGCCGGAATAACGCGCGGAGGTGGTAATCTGTTTGAAGCTGCG 1267  
 Db 1021 ACGCTTCCCGGTCAGCCGGAATAACGCGCGGAGGTGGTAATCTGTTTGAAGCTGCG 1080  
 QY 1268 CGTGGCTTAAAGGATTAACGCGGATGATTCAGGTTTGGCTGCTGCTTCAAGCTTAAAG 1327  
 Db 1081 CGTGGCTTAAAGGATTAACGCGGATGATTCAGGTTTGGCTGCTGCTTCAAGCTTAAAG 1140  
 QY 1328 CAGATGCGTAAAGGATTAACGCGGATGATTCAGGTTTGGCTGCTGCTTCAAGCTTAAAG 1387  
 Db 1141 CAGATGCGTAAAGGATTAACGCGGATGATTCAGGTTTGGCTGCTGCTTCAAGCTTAAAG 1200  
 QY 1388 CTGGCAGATGTAAGAGCGAAATCGCAGGCGATGTTGGTGGCAGGTTTAAAGCAA 1447  
 Db 1201 CTGGCAGATGTAAGAGCGAAATCGCAGGCGATGTTGGTGGCAGGTTTAAAGCAA 1260  
 QY 1448 ATCGTAATGAAGCAGCATACGGCGGTGCAAGTTTGAAT 1487  
 Db 1261 ATCGTAATGAAGCAGCATACGGCGGTGCAAGTTTGAAT 1300

Tue May 4 07:05:30 2004

us-09-866-379d-7.rn1

Page 5

RESULT 5  
US-08-910-798-1  
Sequence 1, Application US/08910798  
Patent No. 5876997  
GENERAL INFORMATION:  
APPLICANT: KREITZ  
TITLE OF INVENTION: NOVEL PHYLASE  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Fish & Richardson P.C.  
STREET: 4225 Executive Square, Suite 1400  
CITY: La Jolla  
STATE: California  
COUNTRY: US  
ZIP: 92037  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/910,798  
FILING DATE: August 13, 1997  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: HAILE, P.D., LISA A.  
REGISTRATION NUMBER: 38,347  
REFERENCE/DOCKET NUMBER: 09010/029001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 619/678-5070  
TELEFAX: 619/678-5099  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1272 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
IMMEDIATE SOURCE:  
CLONE: PHYLASE  
FEATURE:  
NAME/KEY:  
LOCATION:  
US-08-910-798-1

Query Match 61.9%; Score 1175.8; DB 2; Length 1272;  
Best Local Similarity 95.5%; Pred. No. 0;  
Matches 1242; Conservative 0; Mismatches 7; Indels 51; Gaps 1;  
QY 188 ATGAAGCGATCTTATCCCATTTTATCTCTTGATTCGCTTAACCCCGCAATCTGA 247  
DB 1 ATGAAGCGATCTTATCCCATTTTATCTCTTGATTCGCTTAACCCCGCAATCTGA 60  
QY 248 TTCGCTCAGATGAGCCGAGCTGAAGCTGAAGAGTGTGATTCGCTGATGATGAT 307  
DB 61 TTCGCTCAGATGAGCCGAGCTGAAGCTGAAGAGTGTGATTCGCTGATGATGAT 120  
QY 308 GTTCGCTCAGATGAGCCGAGCTGAAGCTGAAGAGTGTGATTCGCTGATGATGAT 367  
DB 121 GTTCGCTCAGATGAGCCGAGCTGAAGCTGAAGAGTGTGATTCGCTGATGATGAT 180  
QY 368 ACCTGCGCGGTAAATCTGCTGATGAGCAACCGCGGTGATGATGATGATGATGAT 427  
DB 181 ACCTGCGCGGTAAATCTGCTGATGAGCAACCGCGGTGATGATGATGATGATGAT 240  
QY 428 GGAATTAACCAAGCGATGCTGATGAGCAAGCTGCTGCTGCTGCTGCTGCTGCTG 487  
DB 241 GGAATTAACCAAGCGATGCTGATGAGCAAGCTGCTGCTGCTGCTGCTGCTGCTG 300  
QY 488 CAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 547  
DB 301 CAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 356

QY 548 GCCTGCGCGCGGTGAGCACTGATGATGATGATGATGATGATGATGATGATGATG 607  
DB 357 -----CGAGCGATGATG 369  
QY 608 TCCAGTCCGATCCGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 667  
DB 370 TCCAGTCCGATCCGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 429  
QY 668 AACGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 727  
DB 430 AACGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 489  
QY 728 CCGCAACCGCGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 787  
DB 490 CCGCAACCGCGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 549  
QY 788 CTTAAACGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 847  
DB 550 CTTAAACGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 609  
QY 848 AAGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 907  
DB 610 AAGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 669  
QY 908 GAGATATTTCTCTGCAACAGCAAGGATGATGATGATGATGATGATGATGATGATG 967  
DB 670 GAGATATTTCTCTGCAACAGCAAGGATGATGATGATGATGATGATGATGATGATG 729  
QY 968 GATTCACACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1027  
DB 730 GATTCACACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 789  
QY 1028 CGCAGCGCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1087  
DB 790 CGCAGCGCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 849  
QY 1088 TTGACGCGCCATTCACCGCAAAACAGGCTATGATGATGATGATGATGATGATGAT 1147  
DB 850 TTGACGCGCCATTCACCGCAAAACAGGCTATGATGATGATGATGATGATGATGAT 909  
QY 1148 TTATGCGCGGACACGATGATGATGATGATGATGATGATGATGATGATGATGATG 1207  
DB 910 TTATGCGCGGACACGATGATGATGATGATGATGATGATGATGATGATGATGATG 969  
QY 1208 ACCTGCTCCGATGACCGGATTAACAGCGCGCGCGGATGATGATGATGATGATG 1267  
DB 970 ACCTGCTCCGATGACCGGATTAACAGCGCGCGCGGATGATGATGATGATGATG 1029  
QY 1268 CGTGGGCTAAGCGATTAACAGCGCGCGCGGATGATGATGATGATGATGATGATG 1327  
DB 1030 CGTGGGCTAAGCGATTAACAGCGCGCGCGGATGATGATGATGATGATGATGATG 1089  
QY 1328 CAGATGCGGTAAATGACCGCTGCTGATTAATACCGCGCGCGGATGATGATGATG 1387  
DB 1090 CAGATGCGGTAAATGACCGCTGCTGATTAATACCGCGCGCGGATGATGATGATG 1149  
QY 1388 CTGCGCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1447  
DB 1150 CTGCGCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1209  
QY 1448 ATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1487  
DB 1210 ATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1249  
RESULT 6  
US-09-489-940/C  
Sequence 940, Application US/09489039A  
Patent No. 6610836  
GENERAL INFORMATION:  
APPLICANT: Gary Breton et. al  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA  
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS



CURRENT FILING DATE: 2001-08-22  
NUMBER OF SEQ ID NOS: 18  
SOFTWARE: Microsoft Office 97  
SEQ ID NO 7  
LENGTH: 2337  
TYPE: DNA  
ORGANISM: Methylobionas 16a  
US-09-934-899-7

Query Match 2.9%; Score 55.2; DB 4; Length 2337;  
Best Local Similarity 50.8%; Pred. No. 3.8e-07;  
Matches 132; Conservative 0; Mismatches 128; Indels 0; Gaps 0;

1622 ATAAACCGTATAGTATAGCGTAACTGTAAAGCGGTGGCGGCTTTATACACCACTT 1681  
DB 2205 ATCCGCTATAGCGTAACTGTAAAGCGGTAAATGACGAACTTCTTCACTGCTT 2146  
QY 1682 GAGATAGCGCTTTAATATGACGCGCTGCTTCCAGCGCTGCAATTGACAACTGAC 1741  
DB 2145 GATGATGAAACGCTGGGTTTACGCGGCACTTGCTGCAAGCGCTGAAATGACCTCCAG 2086  
QY 1742 CTTCTTGGGGGTGTTCAACCCAAAGCGCCACGAGCGCTGTGCGCAAGAGCGCC 1801  
DB 2085 CTTCTTGGGGGTATACGCGCTTCTTACACGACGAAAGGTAGCATGCAATGCTTGC 2026  
QY 1802 CACGACCGCGGATCATCTACCGCCAGCATCGCGCGCTATGCAATCACCAATCGTA 1861  
DB 2026 CATGATCGCGGTGGTGGCGCCCAAGATCGCGCGCAATGATGACATATGTTGTA 1966  
QY 1862 ATGTCGTTCGCCCATTTCCA 1881  
DB 1965 AAAGCTTTCAGTGTCTCCA 1946

## RESULT 10

US-08-956-171E-84/C  
Sequence 84, Application US/08956171E  
Patent No. 6593114

GENERAL INFORMATION:  
APPLICANT: Charles Kunsch

Gil H. Choi  
Patrick S. Dillon  
Craig A. Rosen  
Steven C. Barash

TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences

NUMBER OF SEQUENCES: 5256

CORRESPONDENCE ADDRESS:

ADDRESS: Human Genome Sciences, Inc.

STREET: 9410 Key West Avenue

CITY: Rockville

STATE: Maryland

COUNTRY: USA

ZIP: 20850

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.4MB storage

COMPUTER: HP Vectra 486/33

OPERATING SYSTEM: MSDOS Version 6.2

SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/956,171E  
FILING DATE: 20-Oct-1997  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/009,861  
FILING DATE: January 5, 1996  
APPLICATION NUMBER: 08/781,986  
FILING DATE: January 3, 1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Mark J. Hyman  
REGISTRATION NUMBER: 46,789  
REFERENCE/DOCKET NUMBER: PB248P1  
TELECOMMUNICATION INFORMATION:

TELEPHONE: (240) 314-1224  
TELEFAX: (301) 309-8439  
INFORMATION FOR SEQ ID NO: 84:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5738 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 84:  
US-08-956-171E-84

Query Match 2.7%; Score 51.4; DB 4; Length 5738;  
Best Local Similarity 52.0%; Pred. No. 1.1e-05;  
Matches 115; Conservative 0; Mismatches 106; Indels 0; Gaps 0;

1680 TTGAGATAGCGCTTTAATATGACCGCTGCTTCCAGAGCTGATGCAAACTC 1739  
DB 838 TTCAAAATGACACTTGAATGTACTGCTCTTTTCCATAGTGTCTTTT 779  
QY 1740 ACCTCTTGGCGGTGTTCAAGCCAAACGCGCAACGAGGCTGTGCCAAGACGC 1799  
DB 778 ACTTCATTATATATTTTTCATATCAATTAAGACTATCTTTAATATGACGC 719  
QY 1800 CCGACGCGCGGATCATCTACCGCGAGCATGGGGGTATGCAATCAACGATCG 1859  
DB 718 GCATATATGTTGATCATGATGATTAATTAATGCGGGGTATGCAATTAATATGTCG 659  
QY 1860 TAAATGTCGTTGCGCCATTCAGTAAATGACGATCGATC 1900  
DB 658 TAAGTTATTAACAGATCACTAAATTTTGAACCTTC 618

## RESULT 11

US-09-634-238-28/C  
Sequence 28, Application US/09634238  
Patent No. 6544772

GENERAL INFORMATION:

APPLICANT: Glenn, Matthew

APPLICANT: Hayakkala, Ilkka J.

APPLICANT: Bloksberg, Leonard, N.

APPLICANT: Lubbers, Mark W.

APPLICANT: Dekker, James

APPLICANT: Christenson, Anna C.

APPLICANT: Holland, Ross

APPLICANT: O'Toole, Paul W.

APPLICANT: Reid, Julian R.

APPLICANT: Coolbear, Timothy

TITLE OF INVENTION: Polynucleotides, materials incorporating

FILE REFERENCE: 11000,104301

CURRENT APPLICATION NUMBER: US/09/634,238

CURRENT FILING DATE: 2000-08-08

NUMBER OF SEQ ID NOS: 422

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 28

LENGTH: 2326

TYPE: DNA

ORGANISM: Lactobacillus rhamnosus  
US-09-634-238-28

Query Match 2.2%; Score 41.8; DB 4; Length 2326;  
Best Local Similarity 47.2%; Pred. No. 0.0081;  
Matches 127; Conservative 0; Mismatches 142; Indels 0; Gaps 0;

1631 ATAGTTAGCGGCTTATAGCGGTGCTGCGCGCTTTATACACCAATGAGATAGC 1690  
DB 1937 ATAAACATAGCAATTAACGATGCTGTGCAACATGCTTAACCCGTCGACTGA 1878  
QY 1631 GCCTTATATATGAGCGCTGCTGTTCAGACGTGATGACAAATCACTGCTTGGC 1750  
DB 1877 ACCTAATATTTTACCTGAGCAATTTTAAACTTAATGATGATTAATGCTT 1818  
QY 1751 GATGTTCAAGCAAAAGCGGCAACGAGCGGTGTCACACAGACGCCCGACGCGC 1810

Db 1817 TAATGCTTCCATATTTTSCAGACCACTCCGCTGTTTGGAACTAATCTTG 1758  
Qy 1811 GGATGACTACCGCCGCGATCGCGCCGATGACAAATACAGATCCGAATGCGT 1870  
Db 1757 AACATCAGACAGCTGCTAAACTGGTGTGCTCAAGAAATATGCTGAATTACCG 1698  
Qy 1871 CGCCCATTCAGATTAATGACGATCCGAT 1899  
Db 1697 AGCCCACTCAACAGCTTCAACCACTTGGT 1669

RESULT 12  
US-09-710-794-4/c  
Sequence 4, Application US/09710794  
Patent No. 6573069  
GENERAL INFORMATION:  
APPLICANT: Holloway, James L.  
APPLICANT: Gao, Zeren  
TITLE OF INVENTION: NOVEL CRIB PROTEIN ZMSB1  
FILE REFERENCE: 99-76  
CURRENT APPLICATION NUMBER: US/09/710,794  
CURRENT FILING DATE: 2000-11-09  
PRIORITY FILING DATE: 1999-11-10  
PRIORITY FILING DATE: 1999-11-10  
NUMBER OF SEQ ID NOS: 31  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 4  
LENGTH: 2868  
TYPE: DNA  
ORGANISM: Mus musculus  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (173)...(1219)  
US-09-710-794-4

Query March 2.1k; Score 39.8; DB 4; Length 2868;  
Best Local Similarity 53.2k; Pred. No. 0.041;  
Matches 83; Conservative 0; Mismatches 73; Indels 0; Gaps 0;

Qy 315 CTCGACCAAGCCGACCACTGATGACAGATGTCACCCGACGATGCGCAACTG 374  
Db 353 CTGCTCTCTGCGCTTGTAGTGAAGAGAGGTGTCCTCCCAAGGCGCTCCCGCGGC 294  
Qy 375 CGGTAACAGCGGTGGCTGACACCGGAGGTGAGCTAATGCGCTATCTGGACAT 434  
Db 293 CCACATGCAATGATGTGGGGAAGTCAACCGGCGGCACTGATCATCTCGGCTGTAGGT 234  
Qy 435 ACCAAGCCGACGCTCTGTAGCCGACGATTTGCTGG 470  
Db 233 CCGCAGGTGAGCGCGGCTTCAAGTTCAAGAGCTGG 198

RESULT 13  
US-08-916-421B-1  
Sequence 1, Application US/08916421B  
Patent No. 6503729  
GENERAL INFORMATION:  
APPLICANT: Bult et al.  
TITLE OF INVENTION: Complete Genome Sequence of the Methanogenic Archaeon, Methanococcus  
Patent No. 6503729  
TITLE OF INVENTION: Janaschki  
FILE REFERENCE: P8275  
CURRENT APPLICATION NUMBER: US/08/916,421B  
CURRENT FILING DATE: 1997-08-22  
PRIORITY FILING DATE: 1997-08-22  
PRIORITY FILING DATE: 1996-08-22  
NUMBER OF SEQ ID NOS: 3  
SOFTWARE: Patentin version 3.1  
SEQ ID NO 1  
LENGTH: 1664976  
TYPE: DNA

ORGANISM: Methanococcus Janaschki  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (28222)..(28222)  
OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc\_feature  
LOCATION: (28257)..(28258)  
OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc\_feature  
LOCATION: (84773)..(84773)  
OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc\_feature  
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OTHER INFORMATION: n equals a, t, c, or g  
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NAME/KEY: misc\_feature  
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OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc\_feature  
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OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc\_feature  
LOCATION: (191995)..(191995)  
OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc\_feature  
LOCATION: (231580)..(231580)  
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OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc\_feature  
LOCATION: (234814)..(234814)  
OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc\_feature  
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OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc\_feature  
LOCATION: (309418)..(309418)  
OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc\_feature  
LOCATION: (312837)..(312837)  
OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc\_feature  
LOCATION: (312993)..(312993)  
OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc\_feature  
LOCATION: (319226)..(319226)



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OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (559167)..(559167)
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NAME/KEY: misc feature
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OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (741684)..(741684)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (779455)..(779455)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (779676)..(779676)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (85539)..(85539)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (871619)..(871619)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (1084830)..(1084830)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (1096846)..(1096846)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (1139881)..(1139881)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (1130881)..(1130881)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (1310988)..(1310988)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (1313224)..(1313224)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (1349473)..(1349473)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (1349491)..(1349491)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (1470091)..(1470091)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (1565020)..(1565020)
OTHER INFORMATION: n equals a, t, c, or g
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NAME/KEY: misc feature
LOCATION: (1602912)..(1602912)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (1603734)..(1603734)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (1637998)..(1637998)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (1664854)..(1664854)
OTHER INFORMATION: n equals a, t, c, or g
US-08-916-421B-1

Query Match
Best Local Similarity 55.1%; Score 38.4; DB 4; Length 1664976;
Matches 75; Conservative 0; Mismatches 61; Indels 0; Gaps 0;
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QY 151 ATCATATATGTCAGATATGAAAGCGAAACATATGATGAAAGCGATTTATCCATT 210
Db 1133087 ATCCCTTAATATATATTTATTAATAATTCGGATGAAATTTATCTTCTTATT 1133146
QY 211 TTATCTCTTCGATTCGTTACCCCGCATCTGCTCAGAGTGAAGCGAGCT 270
Db 1133147 TTAGCTTTATGATTCATTTTCATTAATATTTAGTAATGAGCCGCTTATT 1133206
QY 271 GAAGCTGAAGTGTG 286
Db 1133207 AGTTTATGATTAATGTG 1133222
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RESULT 14
US-09-252-991A-11337/c
; Sequence 11337, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OR INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; NUMBER OF SEQ. ID NOS: 33142
; SEQ. ID NO 11337
; LENGTH: 1053
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-11337
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Query Match
Best Local Similarity 51.9%; Score 37.2; DB 4; Length 1053;
Matches 84; Conservative 0; Mismatches 78; Indels 0; Gaps 0;
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QY 1718 CAGACGCTGATGACAACTGACCTCTTGGGGGTTCACGCAAAAGCGCAACGAG 1777
Db 357 CATGCGCTGATGAAAGAAACCATGTCGTCGACGCGGAAGTCGTTCGGCATCCA 298
QY 1778 CAGGCTGTGTCACAAAGAAAGCCCAAGACCGGGGATCACTACCGCAGATCGGCGG 1837
Db 297 CAGTCCGGAATCTGCCGATCCGAGCGCGGGCGCGAGCGCTCGCTCCAGGCTGGCGG 238
QY 1838 CGTATCGAAGATACACGAGATGTAATGTGCTGTCCGCAATTC 1879
Db 237 CGGCAAGCGCTCATCAAGGCTGTCCGAGCTGGCGCTCCCATC 196
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RESULT 15
US-09-252-991A-11293
; Sequence 11293, Application US/09252991A
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Patent No. 6551795  
GENERAL INFORMATION:  
APPLICANT: Marc J. Rubenfield et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
FILE REFERENCE: 107196.136  
CURRENT APPLICATION NUMBER: US/09/252,991A  
CURRENT FILING DATE: 1999-02-18  
PRIOR APPLICATION NUMBER: US 60/074,788  
PRIOR FILING DATE: 1998-02-18  
PRIOR APPLICATION NUMBER: US 60/094,190  
PRIOR FILING DATE: 1998-07-27  
NUMBER OF SEQ ID NOS: 33142  
SEQ ID NO 11293  
LENGTH: 2334  
TYPE: DNA  
ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-11293

Query Match 2.0%; Score 37.2; DB 4; Length 2334;  
Best Local Similarity 51.9%; Pred. No. 0.25; Mismatches 78; Indels 0; Gaps 0;  
Matches 84; Conservative 0;

QY	1718	CAGACGCTGATGACAACTCACTCTTTGGCGGTTCACAGCAAAAGCGCAACAG	1777
DB	552	CATGCGCTGGATGAGAAACCGATGTGTGTGACAGCGGAGTGGTATCGCGATCCA	611
QY	1778	CAGGCTGTGCGCAACAGAACGCCCGACGACCGGCGATCACTACCGCCAGCATCGCGG	1837
DB	612	CAGTCGCGAAGTCCCGATCCCGAGCGCGGCGCGCGACGCTCGCTCCAGCGGTGCGCGG	671
QY	1838	CGTATGACATGACCGCATGCTGATGTGTGCGCCATTG	1879
DB	672	CGGACGCGCGCTACTGAGCTGTCCGCGTCCGCTCCAGTTC	713

Search completed: May 2, 2004, 00:29:07  
Job time : 163.653 secs